



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 130647

TO: Bao-Qun Li
Location: REM/3C18
Art Unit: 1648
Thursday, August 26, 2004

Case Serial Number: 10/016986

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

From: Li, Bao-Qun
Sent: Tuesday, August 24, 2004 4:13 PM
To: STIC-Biotech/ChemLib

Please do the sequence homology and interference search for SEQ ID NO: 155 of Application SN. 10,016,986. Bao Qun Li
Art Unit 1648
Tel. 20904.
REM, 3C18.

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AUG 24 2004
STIC

Point of Contact:

Alexandra Wacławiw

STAFF USE ONLY Technical Info. Specialist
CM1 6A02 Tel: 308-4494

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: 8-26
Date Completed: 8-26
Searcher Prep/Rev. Time: 10
Online Time: 15

Type of Search
NA Sequence: # _____
AA Sequence: # 2
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): Cooper

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:36:03 ; Search time 13.7778 Seconds
(without alignments)
464.634 Million cell updates/sec

Title: US-10-016-986-66
Perfect score: 674
Sequence: 1 LEQSGAEVKFGASVKVSCQ.....PDNYMDVMGKGTIVVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/aa/5A COMB.pcp:*
 - 2: /cgn2_6/ptodata/2/aa/5B COMB.pcp:*
 - 3: /cgn2_6/ptodata/2/aa/6A COMB.pcp:*
 - 4: /cgn2_6/ptodata/2/aa/6B COMB.pcp:*
 - 5: /cgn2_6/ptodata/2/aa/PTUS COMB.pcp:*
 - 6: /cgn2_6/ptodata/2/aa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	674	100.0	124	1	US-08-276-852-66
2	674	100.0	124	1	US-08-899-575-66
3	674	100.0	124	1	US-08-899-575-66
4	674	100.0	124	3	US-08-591-632-1
5	674	100.0	124	4	US-09-611-451-1
6	674	100.0	124	5	PCT-US95-08743-66
7	667	99.0	146	1	US-08-276-852-155
8	667	99.0	146	1	US-08-899-575-155
9	667	99.0	146	1	US-08-899-575-155
10	667	99.0	146	5	PCT-US95-08743-155
11	664	98.5	124	3	US-08-591-632-155
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13	663	98.4	124	3	US-08-591-632-46
14	663	98.4	124	4	US-09-611-451-46
15	660	97.9	124	1	US-08-276-852-67
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100	527	78.2	125	1	US-08-899-575-129

ALIGNMENTS

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RESULT 1
US-08-276-852-66
; Sequence 66, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-66

Query Match 100.0%; Score 674; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEQSGAEVKKPGASVKVSQCSGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQCSGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSK 60
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Db 61 FQDRVTFADTTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Qy 121 IVSS 124
Db 121 IVSS 124

RESULT 2
US-08-899-575-66
; Sequence 66, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-66

Query Match 100.0%; Score 674; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEQSGAEVKKPGASVKVSQCSGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQCSGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSK 60
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Db 61 FQDRVTFADTTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Qy 121 IVSS 124
Db 121 IVSS 124
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STIC-Biotech/ChemLib

130647

From: Li, Bao-Qun
Sent: Tuesday, August 24, 2004 4:10 PM
To: STIC-Biotech/ChemLib

Please do the sequence homology and interference search for SEQ ID NO: 66 of Application Sn. 10/016,986. Thanks.
Bao Qun LI
Art Unit 1648.
Tel. 20904.
REM, 3C18.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-899-575-66

Query Match 100.0%; Score 674; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFPMWGWINPYNGNKEFSK 60
Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
Qy 121 IVSS 124
Db 121 IVSS 124

RESULT 4
US-08-591-632-1
Sequence 1, Application US/08591632
Patent No. 6261558

GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92

TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-632-1

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Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
Qy 121 IVSS 124
Db 121 IVSS 124

RESULT 5
US-09-611-451-1
Sequence 1, Application US/09611451
Patent No. 6395275

GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/611,451
;; FILING DATE: 06-Jul-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/591,632
;; FILING DATE: 2001-10-29
;; APPLICATION NUMBER: US 08/308,841
;; FILING DATE: 19-SEP-1994
;; APPLICATION NUMBER: US 08/233,619
;; FILING DATE: 26-APR-1994
;; APPLICATION NUMBER: US 08/139,409
;; FILING DATE: 19-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: TSRI 332.3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 784-2937
;; TELEFAX: (619) 784-9399
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-611-451-1

Query Match 100.0%; Score 674; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
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DB 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 121 IVSS 124
DB 121 IVSS 124

RESULT 6
PCT-US95-08743-66
;; Sequence 66, Application PC/TUS9508743
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;; NUMBER OF SEQUENCES: 170
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/08743

;; FILING DATE: 11-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/276,852
;; FILING DATE: 18-JUL-1994
;; INFORMATION FOR SEQ ID NO: 66:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-08743-66
Query Match 100.0%; Score 674; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
DB 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 121 IVSS 124
DB 121 IVSS 124

RESULT 7
US-08-276-852-155
;; Sequence 155, Application US/08276852
;; Patent No. 5652138
;; GENERAL INFORMATION:
;; APPLICANT: Burton, Dennis R
;; APPLICANT: Barbas, Carlos F
;; APPLICANT: Lerner, Richard A
;; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;; NUMBER OF SEQUENCES: 170
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; ADDRESSEE: Patent Counsel
;; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
;; CITY: Mail Drop TPC8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/276,852
;; FILING DATE: 18-JUL-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 155:
;; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-155

Query Match 99.0%; Score 667; DB 1; Length 146;
Best Local Similarity 99.2%; Pred. No. 2.2e-60;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYNGNKEFSK 82

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 142

QY 121 IVSS 124
DB 143 IVSS 146

RESULT 8
US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-899-575-155

Query Match 99.0%; Score 667; DB 1; Length 146;
Best Local Similarity 99.2%; Pred. No. 2.2e-60;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYNGNKEFSK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 142

QY 121 IVSS 124
DB 143 IVSS 146

RESULT 9
US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-155

Query Match 99.0%; Score 667; DB 1; Length 146;
Best Local Similarity 99.2%; Pred. No. 2.2e-60;

Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 DB 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 82
 QY 61 FQDRVTTADTSANTAYNELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 83 FQDRVTTADTSANTAYNELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 QY 121 IVSS 124
 DB 143 IVSS 146

RESULT 10
 PCT-US95-08743-155
 ; Sequence 155, Application PC/TUS9508743
 ; GENERAL INFORMATION:
 ; APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/08743
 ; FILING DATE: 11-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/276,852
 ; FILING DATE: 18-JUL-1994
 ; INFORMATION FOR SEQ ID NO: 155:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 146 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US95-08743-155

Query Match 99.0%; Score 667; DB 5; Length 146;
 Best Local Similarity 99.2%; Pred. No. 2.2e-60;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 DB 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 82
 QY 61 FQDRVTTADTSANTAYNELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 83 FQDRVTTADTSANTAYNELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 QY 121 IVSS 124
 DB 143 IVSS 146

RESULT 11
 US-08-591-632-45
 ; Sequence 45, Application US/08591632
 ; Patent No. 6261558
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESS: 10550 No. 639525th Torrey Pines Road, TPC 8
 ; CITY: La Jolla

STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/591,632
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/11907
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,841
 FILING DATE: 19-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/233,619
 FILING DATE: 26-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/139,409
 FILING DATE: 19-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: TSRI 332.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 784-2937
 TELEFAX: (619) 784-9399
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 124 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-591-632-45

Query Match 98.5%; Score 664; DB 3; Length 124;
 Best Local Similarity 97.6%; Pred. No. 3.7e-60;
 Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 QY 61 FQDRVTTADTSANTAYNELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 61 FQDRVTTADTSANTAYNELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 12
 US-09-611-451-45
 ; Sequence 45, Application US/09611451
 ; Patent No. 6395275
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESS: 10550 No. 639525th Torrey Pines Road, TPC 8
 ; CITY: La Jolla

; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/611,451
 ; FILING DATE: 06-JUL-2000
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/591,632
 ; FILING DATE: 2001-10-29
 ; APPLICATION NUMBER: US 08/308,841
 ; FILING DATE: 19-SEP-1994
 ; APPLICATION NUMBER: US 08/233,619
 ; FILING DATE: 26-APR-1994
 ; APPLICATION NUMBER: US 08/139,409
 ; FILING DATE: 19-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSRI 332.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
 US-09-611-451-45

Query Match 98.5%; Score 664; DB 4; Length 124;
 Best Local Similarity 97.6%; Pred. No. 3.7e-60;
 Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVVRQAPGQRFPMWGWNPYNGNKEFSAK 60
 Db 1 LEQSGAEVKKPGASVKVSQASGYRFSHFTVHVVRQAPGQRFPMWGWNPYNGNKEFSAK 60
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 QY 121 IVSS 124
 Db 121 IVSS 124

RESULT 13
 US-08-591-632-46
 ; Sequence 46, Application US/08591632
 ; Patent No. 6261558
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; Patent Counsel
 ; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/591,632
 ; FILING DATE: 19-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/11907
 ; FILING DATE: 19-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,841
 ; FILING DATE: 19-SEP-1994
 ; APPLICATION NUMBER: US 08/233,619
 ; FILING DATE: 26-APR-1994
 ; APPLICATION NUMBER: US 08/139,409
 ; FILING DATE: 19-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSRI 332.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
 US-08-591-632-46

Query Match 98.4%; Score 663; DB 3; Length 124;
 Best Local Similarity 97.6%; Pred. No. 4.7e-60;
 Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVVRQAPGQRFPMWGWNPYNGNKEFSAK 60
 Db 1 LEQSGAEVKKPGASVKVSQASGYRFSHFTVHVVRQAPGQRFPMWGWNPYNGNKEFSAK 60
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 QY 121 IVSS 124
 Db 121 IVSS 124

RESULT 14
 US-09-611-451-46
 ; Sequence 46, Application US/09611451
 ; Patent No. 6395275
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; Patent Counsel
 ; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-Jul-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-611-451-46

Query Match 98.4%; Score 663; DB 4; Length 124;
Best Local Similarity 97.6%; Pred. No. 4.7e-60;
Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
Db 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
QY 61 FQDRVTFADTASANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 61 FQDRVTFADTASANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 15
US-08-276-852-67
; Sequence 67, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-Jul-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-611-451-46

Query Match 98.4%; Score 663; DB 4; Length 124;
Best Local Similarity 97.6%; Pred. No. 4.7e-60;
Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
Db 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
QY 61 FQDRVTFADTASANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 61 FQDRVTFADTASANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 16
US-08-899-575-67
; Sequence 67, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-67

Query Match 97.9%; Score 660; DB 1; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
Db 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
QY 61 FQDRVTFADTASANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 61 FQDRVTFADTASANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 16
US-08-899-575-67
; Sequence 67, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
```

```
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-67

Query Match          97.9%; Score 660; DB 1; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSAK 60
   |||||
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSAK 60
   |||||
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
   |||||
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
   |||||
QY 121 IVSS 124
   |||||
Db 121 IVSS 124
   |||||

RESULT 17
US-08-899-575-67
; Sequence 67, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148

; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-67

Query Match          97.9%; Score 660; DB 1; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSAK 60
   |||||
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSAK 60
   |||||
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
   |||||
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
   |||||
QY 121 IVSS 124
   |||||
Db 121 IVSS 124
   |||||

RESULT 18
PCT-US95-08743-67
; Sequence 67, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-67

Query Match          97.9%; Score 660; DB 5; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSAK 60
   |||||
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSAK 60
   |||||
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
   |||||
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
   |||||
QY 121 IVSS 124
   |||||
Db 121 IVSS 124
   |||||
```

Db 121 IVSS 124
 ||||
 RESULT 19
 US-08-591-632-48
 ; Sequence 48, Application US/08591632
 ; Patent No. 6261558
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/591,632
 ; FILING DATE: 19-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/11907
 ; FILING DATE: 19-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,841
 ; FILING DATE: 19-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/233,619
 ; FILING DATE: 19-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/139,409
 ; FILING DATE: 19-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSRI 332.3
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-591-632-48

Query Match 97.5%; Score 657; DB 3; Length 124;
 Best Local Similarity 96.8%; Pred. No. 1.9e-59;
 Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWNPYNGNKEFSK 60
 Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWNPYNGNKEFSK 60
 Qy 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
 Db 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
 Qy 121 IVSS 124
 ||||
 Db 121 IVSS 124

RESULT 20
 US-08-591-632-49
 ; Sequence 49, Application US/08591632
 ; Patent No. 6261558
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; APPLICANT: Burton, Dennis R.
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/591,632
 ; FILING DATE: 19-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/11907
 ; FILING DATE: 19-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,841
 ; FILING DATE: 19-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/233,619
 ; FILING DATE: 26-APR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/139,409
 ; FILING DATE: 19-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSRI 332.3
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-591-632-49

Query Match 97.5%; Score 657; DB 3; Length 124;
 Best Local Similarity 97.6%; Pred. No. 1.9e-59;
 Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWNPYNGNKEFSK 60
 Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWNPYNGNKEFSK 60
 Qy 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
 Db 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
 Qy 121 IVSS 124
 ||||
 Db 121 IVSS 124

US-09-611-451-49
; Sequence 49, Application US/09611451
; Patent No. 6395275

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard

;; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;; NUMBER OF SEQUENCES: 170
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; ADDRESSEE: Patent Counsel
;; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/276,852
;; FILING DATE: 18-JUL-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-276-852-68

Query Match 97.3%; Score 656; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60

QY 61 FQDRVTFADTDSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
DB 61 FQDRVTFADTDSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120

QY 121 IVSS 124
DB 121 IVSS 124

RESULT 24
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of

;; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
;; STREET: Mail Drop TPC8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/899,575
;; FILING DATE: 24-JUL-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/276,852
;; FILING DATE: 18-JUL-1994
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-899-575-68

Query Match 97.3%; Score 656; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60

QY 61 FQDRVTFADTDSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
DB 61 FQDRVTFADTDSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120

QY 121 IVSS 124
DB 121 IVSS 124

RESULT 25
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA

```
;
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-68

Query Match          97.3%; Score 656; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 60

QY 61 FQDRVTFADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 121 IVSS 124
Db 121 IVSS 124

RESULT 26
PCT-US95-08743-68
; Sequence 68, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
```

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-68

Query Match          97.3%; Score 656; DB 5; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 60

QY 61 FQDRVTFADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 121 IVSS 124
Db 121 IVSS 124

RESULT 27
US-08-591-632-47
; Sequence 47, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Righard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESS: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-3399
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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Qy	121	IVSS	124
Db	121	IVSS	124

RESULT 30

RECORD 30
 US-09-611-451-50
 ; Sequence 50, Application US/69911451
 ; Patent No. 6395275
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; Burton, Dennis R.
 ; Lerner, Richard A.
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/611,451
 ; FILING DATE: 06-Jul-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/591,632
 ; FILING DATE: 2001-10-29
 ; APPLICATION NUMBER: US 08/308,841
 ; FILING DATE: 19-SEP-1994
 ; APPLICATION NUMBER: US 08/233,619
 ; FILING DATE: 26-APR-1994
 ; APPLICATION NUMBER: US 08/139,409
 ; FILING DATE: 19-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSRI 332.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 US-09-611-451-50

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Query Match          97.2%; Score 655; DB 4; Length 124;
Best Local Similarity 97.6%; Pred. NO. 3e-59;
Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy	121	IVSS 124	
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Search completed: August 26, 2004, 13:40:27
Job time : 14.7778 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:36:03 ; Search time 16.2222 Seconds

(without alignments)

464.634 Million cell updates/sec

Title: US-10-016-986-155

Perfect score: 793

Sequence: 1-NEWSWVELEFLSWTFGVHSQ.....PDNYMDVWGKTTIVSS 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued-Patents AA:*

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5: /cgn2_6/prodata/2/1aa/PTUS-COMB.pep:*

6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	100.0	146	1	US-08-276-852-155 Sequence 155, App
2	793	100.0	146	1	US-08-899-575-155 Sequence 155, App
3	793	100.0	146	1	US-08-899-575-155 Sequence 155, App
4	793	100.0	146	5	PCT-US95-08743-155 Sequence 155, App
5	667	84.1	124	1	US-08-276-852-66 Sequence 66, Appl
6	667	84.1	124	1	US-08-899-575-66 Sequence 66, Appl
7	667	84.1	124	3	US-08-591-632-1 Sequence 1, Appl
8	667	84.1	124	4	US-09-611-451-1 Sequence 1, Appl
9	667	84.1	124	5	PCT-US95-08743-66 Sequence 66, Appl
10	667	84.1	124	5	PCT-US95-08743-66 Sequence 45, Appl
11	657	82.8	124	3	US-08-591-632-45 Sequence 45, Appl
12	657	82.8	124	4	US-09-611-451-45 Sequence 45, Appl
13	656	82.7	124	3	US-08-591-632-46 Sequence 46, Appl
14	656	82.7	124	4	US-09-611-451-46 Sequence 46, Appl
15	653	82.3	124	1	US-08-276-852-67 Sequence 67, Appl
16	653	82.3	124	1	US-08-899-575-67 Sequence 67, Appl
17	653	82.3	124	1	US-08-899-575-67 Sequence 67, Appl
18	653	82.3	124	5	PCT-US95-08743-67 Sequence 67, Appl
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20	650	82.0	124	4	US-09-611-451-49 Sequence 49, Appl
21	650	82.0	124	4	US-09-611-451-49 Sequence 49, Appl
22	649	81.8	124	1	US-08-276-852-68 Sequence 68, Appl
23	649	81.8	124	1	US-08-899-575-68 Sequence 68, Appl
24	649	81.8	124	1	US-08-899-575-68 Sequence 68, Appl
25	649	81.8	124	1	PCT-US95-08743-68 Sequence 68, Appl
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27	648	81.7	124	3	US-08-591-632-47 Sequence 47, Appl

28	648	81.7	124	3	US-08-591-632-50 Sequence 50, Appl
29	648	81.7	124	4	US-09-611-451-47 Sequence 47, Appl
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32	646	81.5	124	4	US-09-611-451-5 Sequence 5, Appl
33	645	81.3	124	3	US-08-591-632-3 Sequence 3, Appl
34	645	81.3	124	4	US-09-611-451-3 Sequence 3, Appl
35	641.5	80.9	124	1	US-08-276-852-130 Sequence 130, App
36	641.5	80.9	124	1	US-08-899-575-130 Sequence 130, App
37	641.5	80.9	124	1	US-08-899-575-130 Sequence 130, App
38	641.5	80.9	124	5	PCT-US95-08743-130 Sequence 130, App
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40	635	80.1	124	4	US-09-611-451-2 Sequence 2, Appl
41	622.5	78.5	123	3	US-08-591-632-4 Sequence 4, Appl
42	622.5	78.5	123	4	US-09-611-451-4 Sequence 4, Appl
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45	619	78.1	124	4	US-09-611-451-61 Sequence 61, Appl
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47	618	77.9	124	3	US-08-591-632-59 Sequence 59, Appl
48	618	77.9	124	4	US-09-611-451-59 Sequence 59, Appl
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56	610	76.9	124	3	US-08-591-632-58 Sequence 58, Appl
57	610	76.9	124	4	US-09-611-451-56 Sequence 56, Appl
58	610	76.9	124	4	US-09-611-451-58 Sequence 58, Appl
59	600	75.7	124	4	US-08-591-632-91 Sequence 91, Appl
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62	599	75.5	124	3	US-08-591-632-92 Sequence 92, Appl
63	599	75.5	124	4	US-09-611-451-89 Sequence 89, Appl
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67	572.5	72.2	124	1	US-08-276-852-126 Sequence 126, App
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82	543.5	68.5	125	1	US-08-899-575-128 Sequence 128, App
83	543.5	68.5	125	1	US-08-899-575-124 Sequence 124, App
84	543.5	68.5	125	1	US-08-899-575-128 Sequence 128, App
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86	543.5	68.5	125	5	PCT-US95-08743-128 Sequence 128, App
87	540.5	68.2	124	1	US-08-276-852-127 Sequence 127, App
88	540.5	68.2	124	1	US-08-899-575-127 Sequence 127, App
89	540.5	68.2	124	1	US-08-899-575-127 Sequence 127, App
90	540.5	68.2	124	5	PCT-US95-08743-127 Sequence 127, App
91	536.5	67.7	126	1	US-08-276-852-123 Sequence 123, App
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100	528.5	66.6	139	2	US-08-452-164A-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-276-852-155
; Sequence 155, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-155

Query Match: 100.0%; Score 793; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEWSWFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYSRFSNFIHWVRQAP 60
QY 61 GQRFEMWGINPYNNGNKFSAKFDQRTVTTADTSANTAYMELSLRSADTAVYYCARVGP 120
DB 61 GQRFEMWGINPYNNGNKFSAKFDQRTVTTADTSANTAYMELSLRSADTAVYYCARVGP 120
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DB 121 YSWDDSPQDNYNDVWGKGTIVVSS 146

RESULT 2

US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-155
Query Match: 100.0%; Score 793; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 YSWDDSPQDNYNDVWGKGTIVVSS 146
DB 121 YSWDDSPQDNYNDVWGKGTIVVSS 146
RESULT 3
US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-155

Query Match 100.0%; Score 793; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
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Db 121 YSWDDSPQDNYMDVWGKTTIVSS 146

RESULT 4
PCT-US95-08743-155
Sequence 155, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-155

Query Match 100.0%; Score 793; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Qy 61 GORFEMGWINPYNGKKEFSKQDRVTFTADTSANTAYMELRSADTAVYICARVGP 120
Db 61 GORFEMGWINPYNGKKEFSKQDRVTFTADTSANTAYMELRSADTAVYICARVGP 120
Qy 121 YSWDDSPQDNYMDVWGKTTIVSS 146
Db 121 YSWDDSPQDNYMDVWGKTTIVSS 146

RESULT 5
US-08-276-852-66
Sequence 66, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-276-852-66

Query Match 84.1%; Score 667; DB 1; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAPGQRFQFWMGWINPYNKKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAPGQRFQFWMGWINPYNKKEFSK 60
QY 83 FQDRVTTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRVTTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146
Db 121 IVSS 124

RESULT 6
US-08-899-575-66
Sequence 66, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-66

Query Match 84.1%; Score 667; DB 1; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAPGQRFQFWMGWINPYNKKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAPGQRFQFWMGWINPYNKKEFSK 60
QY 83 FQDRVTTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRVTTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 7
US-08-899-575-66
Sequence 66, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-66

Query Match      84.1%; Score 667; DB 1; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 82
DB 1 LEQSGAEVKKPGASVKSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60

QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 8
US-08-591-632-1
; Sequence 1, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 92
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-591-632-1

Query Match      84.1%; Score 667; DB 3; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 82
DB 1 LEQSGAEVKKPGASVKSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60

QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 9
US-09-611-451-1
; Sequence 1, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 92
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-611-451-1

Query Match      84.1%; Score 667; DB 4; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;

```


STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA: US/09/611,451
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-611-451-45

Query Match 82.8%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 5.9e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKPGASVKSCQASGYRFSNFIHWVRQAPGORFEWGWINPYNKKEFSAK 82
Db 1 LEQSGAEVKPGASVKSCQASGYRFSNFIHWVRQAPGORFEWGWINPYNKKEFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 13
US-08-591-632-46
Sequence 46, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Lerner, Richard A.
Burton, Dennis R.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA: US/08/591,632
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-632-46

Query Match 82.7%; Score 656; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 7.4e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKPGASVKSCQASGYRFSNFIHWVRQAPGORFEWGWINPYNKKEFSAK 82
Db 1 LEQSGAEVKPGASVKSCQASGYRFSNFIHWVRQAPGORFEWGWINPYNKKEFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 14
US-09-611-451-46
Sequence 46, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Lerner, Richard A.
Burton, Dennis R.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-611-451-46

Query Match 82.7%; Score 656; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 7.4e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGNINPYNGKFSK 82
DB 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGNINPYNGKFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
DB 121 IVSS 124

RESULT 15
US-08-276-852-67
Sequence 67: Application US 08/276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-67

Query Match 82.3%; Score 653; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVQSGAEVKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGNINPYNGKFSK 82
DB 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGNINPYNGKFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
DB 121 IVSS 124

RESULT 16
US-08-899-575-67
Sequence 67: Application US 08/899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994

5804.440

APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-67

Query Match 82.3%; Score 653; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEEWGWINPYNNGKFSAK 82
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEEWGWINPYNNGKFSAK 60

QY 83 FQDRVTFDTADTANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFDTADTANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 17
US-08-899-575-67
Sequence 67, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-67

Query Match 82.3%; Score 653; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEEWGWINPYNNGKFSAK 82
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEEWGWINPYNNGKFSAK 60

QY 83 FQDRVTFDTADTANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFDTADTANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 18
PCT-US95-08743-67
Sequence 67, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-67

Query Match 82.3%; Score 653; DB 5; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEEWGWINPYNNGKFSAK 82
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEEWGWINPYNNGKFSAK 60

QY 83 FQDRVTFDTADTANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFDTADTANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146

Db 121 IVSS 124

RESULT 19

US-08-591-632-48
; Sequence 48, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; NAME: Fitting, Thomas
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-48

Query Match 82.0%; Score 650; DB 3; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.9e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 82
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 20

US-08-591-632-49
; Sequence 49, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; NAME: Fitting, Thomas
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-49

Query Match 82.0%; Score 650; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 2.9e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 82
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 21

US-09-611-451-48
; Sequence 48, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; Lerner, Dennis R.
; Burton, Dennis R.
; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel

STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0
CURRENT APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000

PRIOR APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29

APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994

APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-9399

TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-09-611-451-48

Query Match 82.0%; Score 650; DB 4; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.9e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIWHVROAPGQRFVWGMWNPYNGNKEFSK 82

Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFTLQWVRQAPGQRFVWGMWNPYNGNKEFSK 60

QY 83 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 142

Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146

Db 121 IVSS 124

RESULT 22

US-09-611-451-49

; Sequence 49, Application US/09611451

; Patent No. 6395275

;

GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Lerner, Dennis R.
Burton, Dennis R.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel

STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0
CURRENT APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000

PRIOR APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29

APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994

APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:

US-09-611-451-49

Query Match 82.0%; Score 650; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 2.9e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIWHVROAPGQRFVWGMWNPYNGNKEFSK 82

Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFTLQWVRQAPGQRFVWGMWNPYNGNKEFSK 60

QY 83 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 142

Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146

Db 121 IVSS 124

RESULT 23

US-08-276-852-68

; Sequence 68, Application US/08276852

; Patent No. 5652138

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

;; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;; NUMBER OF SEQUENCES: 170
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; ADDRESSEE: Patent Counsel
;; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/276,852
;; FILING DATE: 18-JUL-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-276-852-68

Query Match 81.8%; Score 649; DB 1; Length 124;
Best Local Similarity 95.2%; Pred. No. 3.7e-57;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60

Qy 83 FQDRVTFTADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRVTFTADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTKV 120

Qy 143 IVSS 146
Db 121 IVSS 124

RESULT 24
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel

;; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
;; STREET: Mail Drop TPC8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/899,575
;; FILING DATE: 24-JUL-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/276,852
;; FILING DATE: 18-JUL-1994
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-899-575-68

Query Match 81.8%; Score 649; DB 1; Length 124;
Best Local Similarity 95.2%; Pred. No. 3.7e-57;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60

Qy 83 FQDRVTFTADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRVTFTADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTKV 120

Qy 143 IVSS 146
Db 121 IVSS 124

RESULT 25
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA

MOLECULE TYPE: protein

US-08-591-632-47

Query Match 81.7%; Score 648; DB 3; Length 124;

Best Local Similarity 96.8%; Pred. No. 4.6e-57;

Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKYSQCOASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSAK 82

DB 1 LEQSGAEVKKPGASVKYSQCOASGYRFSHFITIMVRQAPGQRFEMWGWINPYNKKEFSAK 60

QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142

DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146

DB 121 IVSS 124

RESULT 28

US-08-591-632-50

; Sequence 50, Application US/08591632

; Patent No. 6261558

; GENERAL INFORMATION:

; APPLICANT: Barbas, Carlos F.

; APPLICANT: Burton, Dennis R.

; APPLICANT: Lerner, Richard A.

; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 92

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/591,632

; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/11907

; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/308,841

; FILING DATE: 19-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/233,619

; FILING DATE: 26-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/139,409

; FILING DATE: 19-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: TSRI 332.3

; TELEPHONE: (619) 784-2937

; TELEFAX: (619) 784-9399

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-591-632-50

Query Match 81.7%; Score 648; DB 4; Length 124;

Best Local Similarity 96.8%; Pred. No. 4.6e-57;

Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Query Match

Best Local Similarity 96.8%; Pred. No. 4.6e-57;

Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKYSQCOASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSAK 82

DB 1 LEQSGAEVKKPGASVKYSQCOASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSAK 60

QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142

DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146

DB 121 IVSS 124

RESULT 29

US-09-611-451-47

; Sequence 47, Application US/09611451

; Patent No. 6395275

; GENERAL INFORMATION:

; APPLICANT: Barbas, Carlos F.

; APPLICANT: Burton, Dennis R.

; APPLICANT: Lerner, Richard A.

; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 92

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/611,451

; FILING DATE: 06-Jul-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/591,632

; FILING DATE: 2001-10-29

; APPLICATION NUMBER: US 08/308,841

; FILING DATE: 19-SEP-1994

; APPLICATION NUMBER: US 08/233,619

; FILING DATE: 26-APR-1994

; APPLICATION NUMBER: US 08/139,409

; FILING DATE: 19-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: TSRI 332.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 784-2937

; TELEFAX: (619) 784-9399

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-611-451-47

Query Match

Best Local Similarity 96.8%; Pred. No. 4.6e-57;

Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:57 ; Search time 32.6074 Seconds
(without alignments)
1199.858 Million cell updates/sec

Title: US-10-016-986-66

Perfect score: 674

Sequence: 1 LQSGAEVKKPGASVKVSCQ.....PDNYMVMWKGTTIVSS 124

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPREMBL 25:

1: sp.archaea:

2: sp.bacteria:

3: sp.fungi:

4: sp.human:

5: sp.invertebrate:

6: sp.mammal:

7: sp.mhc:

8: sp.organelle:

9: sp.phage:

10: sp.plant:

11: sp.rodent:

12: sp.virus:

13: sp.vertibrate:

14: sp.unclassified:

15: sp.rvirus:

16: sp.bacteriaph:

17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	431	63.9	614	4	Q96GA6
2	413.5	61.4	500	4	Q93EV0
3	403.5	59.9	159	4	Q9QSO0
4	392	58.2	119	5	Q9GYZ2
5	390	57.9	119	4	Q9UL94
6	389.5	57.8	124	4	Q9UL92
7	388	57.6	497	4	Q8WY24
8	387	57.4	125	4	Q9UL95
9	383.5	56.9	469	4	Q727P5
10	378.5	56.2	116	4	Q9UL89
11	366.5	54.4	613	11	Q8VCCX7
12	366	54.3	168	11	Q8VDC9
13	366	54.3	468	11	Q99L31
14	363	53.9	470	11	Q7TMK1
15	354.5	52.6	109	11	Q9UL75
16	354.5	52.6	145	11	Q924R3
17	354	52.5	354	11	Q924Q1
18	352.5	52.3	143	11	Q924R0
19	352	52.2	144	11	Q924P5
20	348.5	51.7	143	11	Q924Q5
21	348	51.6	481	11	Q91WT1
22	347.5	51.6	145	11	Q924R4
23	347	51.5	117	11	Q9QXF0
24	347	51.5	147	11	Q925S3
25	346.5	51.4	278	11	Q921K1
26	346	51.3	117	11	Q9QXE9
27	346	51.3	150	4	Q922S8
28	345	51.2	146	11	Q924Q3
29	345	51.2	489	11	Q8VCK4
30	344.5	51.1	143	11	Q91V67
31	343.5	51.0	145	11	Q924Q6
32	342.5	50.8	145	11	Q924Q7
33	342.5	50.8	145	11	Q924R1
34	342	50.7	146	11	Q924R8
35	341.5	50.7	482	11	Q8K172
36	341.5	50.7	488	11	Q8K0F2
37	340.5	50.5	241	11	Q921A6
38	339	50.3	473	11	Q9D814
39	338.5	50.2	145	11	Q924Q9
40	338	50.1	140	11	Q924P8
41	337.5	50.1	143	11	Q924R7
42	337.5	50.1	473	11	Q99125
43	336	49.9	140	11	Q924R2
44	336	49.9	484	11	Q991A6
45	335.5	49.8	141	11	Q924Q4
46	335.5	49.8	145	11	Q924P7
47	333	49.4	123	11	Q8VJ11
48	332.5	49.3	143	11	Q91VA2
49	332	49.2	480	11	Q8K0Z4
50	331.5	49.2	137	11	Q924R6
51	331.5	49.2	143	11	Q924Q0
52	329.5	48.9	118	11	Q921C4
53	328.5	48.7	488	11	Q91WR1
54	328	48.7	170	11	Q925S2
55	325.5	48.3	143	11	Q924P9
56	325	48.2	146	11	Q924Q8
57	324.5	48.1	114	11	Q9JL81
58	324	48.1	157	4	Q95978
59	322.5	47.8	136	11	Q7TPE3
60	321.5	47.7	463	11	Q91C4
61	321	47.6	142	11	Q924Q2
62	320.5	47.6	110	11	Q9JL77
63	320.5	47.6	496	4	Q96DK0
64	319.5	47.4	243	11	Q7TQM2
65	319	47.3	120	11	Q920E8
66	318.5	47.3	481	11	Q8VCV5
67	316.5	47.0	143	11	Q924P6
68	315	46.7	614	11	Q7TMT6
69	314.5	46.7	139	11	Q924R5
70	311	46.1	474	11	Q8R3H6
71	310	46.0	109	11	Q9JL85
72	308	45.7	481	11	Q91WT3
73	306.5	45.5	218	11	Q925S1
74	304	45.1	121	11	Q8CGS2
75	298	44.2	117	11	Q921C6
76	297.5	44.1	110	11	Q9JL83
77	293	43.5	479	11	Q91WP5
78	291	43.2	111	11	Q9D9B8
79	289.5	43.0	613	4	Q8WU11
80	286.5	42.5	573	4	Q8WU38
81	283.5	42.1	298	11	Q9QYF0
82	283.5	42.1	484	11	Q8VEA0
83	280	41.5	499	4	Q8NSK4
84	278	41.2	113	4	Q9UL90
85	274.5	40.7	147	4	Q9Y509
86	273	40.5	116	4	Q9UL93
87	268	39.8	482	4	Q7Z351
88	268	39.8	487	11	Q80Z17
89	268	39.8	597	4	Q96B59

Q8nc16 homo sapien
Q9ixel1 mus musculus
Q9hcc1 homo sapien
Q9ul84 homo sapien
Q91205 mus musculus
Q9ul71 homo sapien
Q91179 mus musculus
Q920e7 mus musculus
Q8n4y9 homo sapien
Q8wux4 homo sapien
Q9bul0 homo sapien

ALIGNMENTS

RESULT 1
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6; 614 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=B-cell;
RA Strausberg R.;
BL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AA009851.1; -;
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EP536E77AA9BBB CRC64;

Query Match 63.9%; Score 431; DB 4; Length 614;
Best Local Similarity 66.1%; Pred. No. 8.6e-38;
Matches 82; Conservative 11; Mismatches 25; Indels 6; Gaps 1;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKFEPSAK 60
DB 23 LVQSGAEVMSPCASVRVSKTSGYAFHTYSLIHWVRQAPGQGLEWMGWISPSDDNTRFAKK 82
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FQDRVTITRDSNMNTAYMELSLRSLEDTAVYICARGYSYSSWDDA-----FDIWGGQTMV 136
QY 121 IVSS 124
DB 137 TVSS 140

RESULT 2
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AA005951.1; -;
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 61.4%; Score 413.5; DB 4; Length 500;
Best Local Similarity 66.4%; Pred. No. 5.2e-36;
Matches 83; Conservative 8; Mismatches 33; Indels 1; Gaps 1;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKFEPSAK 60
DB 23 LVQSGAEVMSPCASVRVSKTSGYAFHTYSLIHWVRQAPGQGLEWMGWISPSDDNTRFAKK 82
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKTT 119
DB 83 FQDRVTITRDSNMNTAYMELSLRSLEDTAVYICARRYCSYSSQNDYIYYMDVWGKTT 142
QY 120 TVSS 124
DB 143 TVSS 147

RESULT 3
Q96QSO PRELIMINARY; PRT; 159 AA.
AC Q96QSO
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 59.9%; Score 403.5; DB 4; Length 159;
Best Local Similarity 63.0%; Pred. No. 1.5e-35;
Matches 80; Conservative 15; Mismatches 29; Indels 3; Gaps 1;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKFEPSAK 60
DB 23 LVQSGAEVMSPCASVRVSKTSGYAFHTYSLIHWVRQAPGQGLEWMGWISPSDDNTRFAKK 82

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QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNY---MDVWGKG 117
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FQGLTWTTRDTSTVTYMDLSLRSDDTAVYFCAREMEITFGGAVSGFYIYGWDYWGQG 142
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 TTVIVSS 124
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 TTVTVSS 149
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TREMELrel. 15, Created)
DT 01-MAR-2001 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.C., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FAGAB CRC64;

Query Match 58.2%; Score 392; DB 5; Length 119;
Best Local Similarity 60.5%; Pred. No. 1.9e-34;
Matches 75; Conservative 20; Mismatches 21; Indels 8; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNKKEFSAK 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LVESGAEVKKPGASVRSCKASGYTFTGYMHWVRQAPGQGLEWIGVNPISRGYTYNQK 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 FQDRVTMTDKSFSTAYMDLSLRSADSAVYICARY---YD-----DHYCLDYWGQGTIV 115
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 TVSS 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 57.8%; Score 389.5; DB 4; Length 124;
Best Local Similarity 61.7%; Pred. No. 3.7e-34;
Matches 79; Conservative 12; Mismatches 26; Indels 11; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNKKEFSAK 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTSSYYMHWVRQAPGQGLEWVGIIINFGGTSYAK 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; RAD56256.1; -.
DR HSSP; P01810; 2FB0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 57.9%; Score 390; DB 4; Length 119;
Best Local Similarity 61.3%; Pred. No. 3.1e-34;
Matches 76; Conservative 12; Mismatches 28; Indels 8; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNKKEFSAK 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWVGIIINFGGTSYAK 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 FQGLTWTTRDTSTAYMELSLRSDDTAVYICARGG-----GRGLWDFPGQGTIV 115
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 TVSS 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 57.8%; Score 389.5; DB 4; Length 124;
Best Local Similarity 61.7%; Pred. No. 3.7e-34;
Matches 79; Conservative 12; Mismatches 26; Indels 11; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNKKEFSAK 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTSSYYMHWVRQAPGQGLEWVGIIINFGGTSYAK 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARV-----VGPVSWDDSPQDNYMDVWGK 116
RT 64 FQGRVTFADTSANTAYMELSLRSADTAVYCARV-----VGPVSWDDSPQDNYMDVWGK 116
DB 64 FQGRVTFADTSANTAYMELSLRSADTAVYCARV-----VGPVSWDDSPQDNYMDVWGK 116
QY 117 GTTVIVSS 124
DB 117 GTTVIVSS 124

RESULT 7
Q8WY24 Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Zeng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RA "Identification and characterization of SMC66, a Ig-like gene which is
RT down-regulated in colorectal cancer."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF283666; AAL36987.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SMC0406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 5365 MW; F24D08DFA5A663E5 CRC64;

Query Match 57.6%; Score 388; DB 4; Length 497;
Best Local Similarity 58.8%; Pred. No. 2.9e-33;
Matches 77; Conservative 12; Mismatches 26; Indels 16; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNVFHWVROAPGQRFWMGWINPYNGKKEFSK 60
DB 23 LEQSGAEVKKPGASVKVSCQASGYRFSNVFHWVROAPGQRFWMGWINPYNGKKEFSK 60
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARV-----PYSWDDSPQDNYMDV 113
DB 83 FQGRVTFADTSANTAYMELSLRSADTAVYCARV-----PYSWDDSPQDNYMDV 113
QY 114 WKGKGTIVSS 124
DB 134 WKGKGTIVSS 124

RESULT 8
Q9UL95 Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DB (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;

"MYOSIN-reactive autoantibodies in rheumatic carditis and normal fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -.
DR HSP; P01810; 2FBJ
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMC0406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; OD3CD5C232488EAC CRC64;

Query Match 57.4%; Score 387; DB 4; Length 125;
Best Local Similarity 61.3%; Pred. No. 7e-34;
Matches 76; Conservative 14; Mismatches 32; Indels 2; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNVFHWVROAPGQRFWMGWINPYNGKKEFSK 60
DB 4 LIVESGAEVKKPGASVKVSCQASGYRFSNVFHWVROAPGQRFWMGWINPYNGKKEFSK 63
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARV-----PYSWDDSPQDNYMDV 120
DB 64 FQGRVTFADTSANTAYMELSLRSADTAVYCARV-----PYSWDDSPQDNYMDV 121
QY 121 IVSS 124
DB 122 TVSS 125

RESULT 9
QZ77P5 QZ77P5 PRELIMINARY; PRT; 469 AA.
AC QZ77P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice.
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC051328; AAH51328.1; -.

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KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C9D5BE12BAAF795C CRC64;

Query Match      56.9%; Score 383.5; DB 4; Length 469;
Best Local Similarity 58.1%; Pred. No. 8.2e-33;
Matches 75; Conservative 17; Mismatches 20; Indels 17; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMGINPYNGNKEFSK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LVQSGAEVKKPGASVKLSCKTSGYFSSYDLIWRQAPGQGLEWGMGWSAHNGDTYARK 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCA-----RVGPYSWDDSPQDNYMDVWG 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FQGRVTWTTDSATTSYMEFSLRSDDTALFYCATKSRGQGVDF-----DSWG 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 KGTIVVSS 124
Db 131 QGLTVVSS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 116
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match      56.2%; Score 378.5; DB 4; Length 116;
Best Local Similarity 62.9%; Pred. No. 5.2e-33;
Matches 78; Conservative 10; Mismatches 25; Indels 11; Gaps 2;

QY 3 QSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMGINPYNGNKEFSK 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 QSGAEVKKPGSSVKVSCASGGTFSSYALSWVRQAPGQGLEWGMRIPIILGIANVAQKFQ 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 DRVTFVTADTSANTAYMELSLRSADTAVYYCA--RVGPYSWDDSPQDNYMDVWGKTTV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 GRVTITADKSTAYMELSLRSADTAVYYCASSNWGPY-----WFDLWGRGTLV 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
Db 113 TVSS 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7
AC Q8VCX7;

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein.
GN IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR MGD; MGI:96448; Igh-6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match      54.4%; Score 366.5; DB 11; Length 613;
Best Local Similarity 56.8%; Pred. No. 7.7e-31;
Matches 71; Conservative 20; Mismatches 23; Indels 11; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMGINPYNGNKEFSK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LQSGAELMKPGASVKISKATGYTFSSYWIWKVQKRGHLEWIGELTPGSGSTNYNEK 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCA--RVGPYSWDDSPQDNYMDVWGKTT 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 PKGATFTADTSSNTAYMQLSLTSEDSAVYYCARRLG-----RWTFDVMGAGTT 132
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 VIVSS 124
Db 133 VIVSS 137
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q8VDC9 PRELIMINARY; PRT; 168 AA.
AC Q8VDC9;
DR 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Anti-MOG 212 variable gamma 2a (Fragment).
GN IGG2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembli P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416332; CAC94867.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

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FT NON TER 168 168
SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E27223 CRC64;

Query Match
Best Local Similarity 54.3%; Score 366; DB 11; Length 168;
Matches 69; Conservative 18; Mismatches 29; Indels 8; Gaps 1;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 23 LQSGAELEKPGASVKLSCKATGYTSSYWDVAVKQRPQGLWIGLEILPGSGRTYINEX 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FQKRTTFTADTSNTAYIQSSLTSDSAVYICANYGSSRW-----YFDVWGAGTTV 134
QY 121 IVSS 124
DB 135 TVSS 138

RESULT 13
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -
DR PDB; 2AP2; 24-NOV-99
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SMC0406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 963523228B3332ADB CRC64;

Query Match
Best Local Similarity 54.0%; Score 366; DB 11; Length 468;
Matches 67; Conservative 22; Mismatches 27; Indels 8; Gaps 1;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 23 LQSGAELEKPGASVKLSCKATGYTSSYWDVAVKQRPQGLWIGLEILPGSGRTYINEX 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FQKRTTFTADTSNTAYIQSSLTSDSAVYICARNLLYGG-----YYDYWGQGTII 134
QY 121 IVSS 124
DB 135 TVSS 138

RESULT 14
Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZEC II; TISSUE=Breast tumor;
RX MEDLINE=2238825; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZEC II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AA055910.1; -
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896B090 CRC64;

Query Match
Best Local Similarity 53.9%; Score 363; DB 11; Length 470;
Matches 68; Conservative 22; Mismatches 28; Indels 6; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 23 LQSGAELEKPGASVKLSCKATGYTGYMHWKQSGKSLWIGLVNPSNGDTSNQK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FQKRTTFTADTSNTAYMELSLTSDSAVYICAR---YYVSGS---YVYFDVWGAGTTV 136
QY 121 IVSS 124
DB 137 TVSS 140

RESULT 15
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C.
RX MEDLINE=2044942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;

Query Match
Best Local Similarity 52.6%; Score 354.5; DB 11; Length 145;
Matches 67; Conservative 23; Mismatches 27; Indels 7; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVHVRQAPQGRPEWMMGWINPYNGNKEFSK 60
Db 4 LQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKRQPGGLEWIGRIDPNSGGTYNKEK 63
QY 61 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 64 FKSATLTVDKSSSTAYMQLSLTSDSAVYCAR-GLY-----DGNWYFDVWGKGTIV 116
QY 121 IVSS 124
Db 117 TVSS 120

RESULT 17
Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63929.1; -.
DR PIR; F33932; F33932.
DR PIR; I28833; I28833.
DR PIR; PH156; PH156.
DR PIR; PH158; PH158.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match
Best Local Similarity 52.5%; Score 354; DB 11; Length 142;
Matches 67; Conservative 21; Mismatches 26; Indels 10; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVHVRQAPQGRPEWMMGWINPYNGNKEFSK 60
Db 4 LQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKRQPGGLEWIGRIDPNSGGTYNKEK 63
QY 61 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 64 FKSATLTVDKSSSTAYMQLSLTSDSAVYCAR-GLY-----DGNWYFDVWGKGTIV 113
QY 121 IVSS 124

with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206031; AAF69329.1; -.
DR PIR; S26312; S26312.
DR PIR; S26313; S26313.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match
Best Local Similarity 52.8%; Score 354.5; DB 11; Length 109;
Matches 65; Conservative 21; Mismatches 23; Indels 9; Gaps 1;

QY 7 EVKPGASVKVSCQASGYRFSNFIHVHVRQAPQGRPEWMMGWINPYNGNKEFSKAFQDRV 66
Db 1 ELVPGASVKVSCKASGYTFTSYMMHWVKRQPGGLEWIGRIDPNSGGTYNKEKFKGAT 60
QY 67 FTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIVVSS 124
Db 61 LTSKSSSTAYMELSLTSDSAVYCAR-GLY-----FDYWGQGTITLVSS 109

RESULT 16
Q924R3 PRELIMINARY; PRT; 145 AA.
AC Q924R3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V186.2-D-J-C mu protein (Fragment).
GN V186.2-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067787; BAB63272.1; -.
DR PIR; F28833; F28833.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH129; PH129.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH144; PH144.
DR PIR; PH147; PH147.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.
DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR PIR; S26744; S26744.
DR InterPro; IPR007110; Ig-like.

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Db      114 TVSS 117
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RESULT 18
Q924R0 PRELIMINARY; PRT; 143 AA.
AC Q924R0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067790; BAB63275.1; -.
DR PIR: F28833; F28833.
DR PIR: F33932; F33932.
DR PIR: PH1105; PH1105.
DR PIR: PH1108; PH1108.
DR PIR: PH1114; PH1114.
DR PIR: PH1118; PH1118.
DR PIR: PH1119; PH1119.
DR PIR: PH1125; PH1125.
DR PIR: PH1126; PH1126.
DR PIR: PH1128; PH1128.
DR PIR: PH1129; PH1129.
DR PIR: PH1131; PH1131.
DR PIR: PH1134; PH1134.
DR PIR: PH1137; PH1137.
DR PIR: PH1139; PH1139.
DR PIR: PH1142; PH1142.
DR PIR: PH1144; PH1144.
DR PIR: PH1147; PH1147.
DR PIR: PH1149; PH1149.
DR PIR: PH1150; PH1150.
DR PIR: PH1151; PH1151.
DR PIR: PH1152; PH1152.
DR PIR: PH1153; PH1153.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMC0406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15968 MW; 13982E966B81E07F CRC64;

Query Match 52.3%; Score 352.5; DB 11; Length 143;
Best Local Similarity 52.4%; Pred. No. 4.3e-30;
Matches 65; Conservative 26; Mismatches 24; Indels 9; Gaps 2;

Qy 1 LEQGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LQPGAEVLKPGASVKLSCKASGYTFTSYWVHWKQRPGRGLEWIGRIDPNSGGTKYNEK 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 FQDRVTFTADTSANTAYNELRLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 FSKATLTVDKPSSTAYNQLSLTSDSAVYYCAR-----WD----EDYMDVWGKTSV 114
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 121 IVSS 124
|||
Db 115 TVSS 118
||||

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RESULT 19
Q924P5 PRELIMINARY; PRT; 144 AA.
AC Q924P5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB069920; BAB63936.1; -.
DR PIR: PH1137; PH1137.
DR PIR: S26744; S26744.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMC0406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;

Query Match 52.2%; Score 352; DB 11; Length 144;
Best Local Similarity 52.4%; Pred. No. 4.9e-30;
Matches 65; Conservative 22; Mismatches 29; Indels 8; Gaps 1;

Qy 1 LEQGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LQPGAEVLKPGASVKLSCKASGYTFTSYWVHWKQRPGRGLEWIGRIDPNSGGTKYNEK 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 FQDRVTFTADTSANTAYNELRLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 FSKATLTVDKPSSTAYNQLSLTSDSAVYYCASYSYV-----YFDVWGKTTV 115
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 121 IVSS 124
|||
Db 116 TVSS 119
||||

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RESULT 20
Q924Q5 PRELIMINARY; PRT; 143 AA.
AC Q924Q5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067795; BAB63280.1; -.
DR PIR: F28833; F28833.
DR PIR: PH1105; PH1105.

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DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match      51.7%; Score 348.5; DB 11; Length 143;
Best Local Similarity 52.4%; Pred. No. 1.2e-29;
Matches 65; Conservative 22; Mismatches 28; Indels 9; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
DB 4 LQSGAEVKKPGASVKLSCKASGYTFTSYIHWVQRPGQLGWIGWYIPGDGNTKYN 63
QY 61 FQDRVFTTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGK 120
DB 64 FSKSKALTVDKPSSTAYMQLSSTSDSAVYICARFYDYE-----YFDVWG 114
QY 121 IVSS 124
DB 115 TVSS 118

RESULT 21
ID Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067785; BAB63270.1; -
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 481
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

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Query Match      51.6%; Score 348; DB 11; Length 481;
Best Local Similarity 52.4%; Pred. No. 5.7e-29;
Matches 65; Conservative 23; Mismatches 26; Indels 10; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
DB 23 LQSGAEVKKPGASVKLSCKASGYTFTSYIHWVQRPGQLGWIGWYIPGDGNTKYN 82
QY 61 FQDRVFTTADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGK 120
DB 83 FKGKTTLTADKSSSTAYMFLSSLTSDSAVYICARVGGWAF-----DYWG 132
QY 121 IVSS 124
DB 133 TVSS 136

RESULT 22
ID Q924R4 PRELIMINARY; PRT; 145 AA.
AC Q924R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067785; BAB63270.1; -
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16081 MW; ECDB1A135E05B88A CRC64;

Query Match      51.6%; Score 347.5; DB 11; Length 145;
Best Local Similarity 52.4%; Pred. No. 1.5e-29;

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Matches 65; Conservative 25; Mismatches 27; Indels 7; Gaps 2;
QY 1 LEQGAELVPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNKKEFSK 60
Db 4 LQPGAEVLVPGASVKLSCKASGYTTSYWMHWKQRPFGGLEWIRIPNSGGTKYNEK 63
QY 61 FQDRTVTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Db 64 FKSKATLTVKPSSTAYMQLSLTSDSAVYCAR-SDYDYD-----YAMDYWGQGTSTV 116
QY 121 IVSS 124
Db 117 TVSS 120

RESULT 23
Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ25171; CAB65236.1; -
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47B4C CRC64;

Query Match 51.5%; Score 347; DB 11; Length 117;
Best Local Similarity 51.6%; Pred. No. 1.3e-29;
Matches 64; Conservative 23; Mismatches 27; Indels 10; Gaps 1;
QY 1 LEQGAELVPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNKKEFSK 60
Db 4 LQSGPELVPGASVKVSCASGYTFDYKWKVKQSHGKSLWIGDIPNNGGTSYNOK 63
QY 61 FQDRTVTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Db 64 FKSKATLTVKPSSTAYMQLSLTSDSAVYCAR-----DKDYFYDYGQGTTL 113
QY 121 IVSS 124
Db 114 TVSS 117

RESULT 24
Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 51.5%; Score 347; DB 11; Length 147;
Best Local Similarity 55.6%; Pred. No. 1.7e-29;
Matches 69; Conservative 17; Mismatches 30; Indels 8; Gaps 2;
QY 1 LEQGAELVPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNKKEFSK 60
Db 6 LQSGPELVPGASVKLSCKASGYTTSYDIDWVRQTPQGLEWIGWIFGEGSTYNEK 65
QY 61 FQDRTVTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Db 66 FKGRATLVKSSSTAYMELTSLTSDSAVYFCAR-GDYY-----RRIFDLWGQGTTV 117
QY 121 IVSS 124
Db 118 TVSS 121

RESULT 25
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAI12207.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 51.4%; Score 346.5; DB 11; Length 278;
Best Local Similarity 53.2%; Pred. No. 4.2e-29;
Matches 66; Conservative 21; Mismatches 30; Indels 7; Gaps 2;
QY 1 LEQGAELVPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNKKEFSK 60
Db 23 LQPGAEVLVPGASVKLSCKASGYTTSYWMHWKQRPFGGLEWIRIPNSGGTSYNOK 82

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DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 51.2%; Score 345; DB 11; Length 146;
Best Local Similarity 52.4%; Pred. No. 2.8e-29;
Matches 65; Conservative 25; Mismatches 28; Indels 6; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYGNKEFSK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LQPGAEIVRPGETSVKLSCKASGYTFTSYWVHWKQRPGRGLEWIGRIDPNSGGTKYNEK 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFATDSANTAYNELRSADTAVYVCARVGPYSWDDSPQDNYMDVWVGKTTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 FKSKATLVTDPSPSTAYNQSLTSDSAVYFCAR-SLYDYG-----YMDYWGQGTSV 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
   |||
Db 118 TVSS 121
   |||

RESULT 29
Q8VCX4 PRELIMINARY; PRT; 489 AA.
AC Q8VCX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein.
GN IGH-VJ558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAI18322.1; -.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IGH_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IGH_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;

Query Match 51.2%; Score 345; DB 11; Length 489;
Best Local Similarity 50.4%; Pred. No. 1.2e-28;
Matches 65; Conservative 23; Mismatches 29; Indels 12; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYGNKEFSK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LQSGAEIVRPGETSVKLSCKASGYTFTSYWVHWKQRPGRGLEWIGRIDPNSGGTKYNEK 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFATDSANTAYNELRSADTAVYVCARVGPYSWDDSPQDNYMDVWVGKTTV 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FKDKATLTDKSTTVYMDLSRLTSDSAVYFCAR-----HEDRGNYDGSILAWFVYWG 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 116 KGTTVIVSS 124
   |||:|||||:
Db 136 QGTLVTYSA 144
   |||:|||||:

RESULT 30
Q91V67 PRELIMINARY; PRT; 143 AA.
ID Q91V67;
AC Q91V67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHS6.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN V304-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -.
DR EMBL; AB069914; BAB63930.1; -.
DR PIR; S26744; S26744.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

Query Match 51.1%; Score 344.5; DB 11; Length 143;
Best Local Similarity 51.6%; Pred. No. 3.1e-29;
Matches 64; Conservative 23; Mismatches 28; Indels 9; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYGNKEFSK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LQPGAEIVRPGETSVKLSCKASGYTFTSYWVHWKQRPGRGLEWIGVIDSDSYTNQK 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFATDSANTAYNELRSADTAVYVCARVGPYSWDDSPQDNYMDVWVGKTTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 FKSKATLVTDPSTSTAYNQSLTSDSAVYCA-----PTVDDWYFDVWVGTTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
   |||
Db 115 TVSS 118
   |||

Search completed: August 26, 2004, 13:39:23
Job time : 38.6074 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:34:32 ; Search time 11.9407 Seconds
(without alignments)
998.912 Million cell updates/sec

Title: US-10-016-986-66

Perfect score: 674

Sequence: 1 LKQSGAEVKKPGASVKVSQ.....PDNYMDVWGKGTIVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR-78:

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1.	433	67.2	129	2 S36260	Ig heavy chain V r
2	449	66.6	129	2 S46393	Ig heavy chain V r
3	433.5	64.3	118	2 PH1666	Ig heavy chain V r
4	432.5	64.2	124	2 S19665	Ig heavy chain V r
5	423.5	62.8	114	2 PH1667	Ig heavy chain V r
6	419	62.2	148	2 S29257	Ig heavy chain V r
7	417	61.9	123	2 S33548	Ig heavy chain V-1
8	416.5	61.8	118	2 S36265	Ig heavy chain V r
9	413	61.3	133	2 C33548	Ig heavy chain V-1
10	413	61.3	627	2 S14683	Ig mu chain precur
11	408	60.5	127	2 PH0955	Ig heavy chain V r
12	402.5	59.7	136	2 S31600	Ig heavy chain V r
13	402.5	59.7	143	1 E1HUND	Ig heavy chain pre
14	400	59.3	122	2 S46394	Ig heavy chain V r
15	398.5	59.1	132	2 S18553	Ig heavy chain V r
16	397	58.9	117	2 S34014	Ig heavy chain V r
17	396	58.8	127	2 B33548	Ig heavy chain V-1
18	395.5	58.7	136	2 PH0954	Ig heavy chain V r
19	395.5	58.7	132	2 S49530	anti-Sm antibody V
20	395.5	58.7	135	2 S49530	Ig heavy chain V r
21	394	58.5	121	2 A49590	Ig heavy chain V r
22	393.5	58.4	171	2 S23623	Ig heavy chain V r
23	392.5	58.2	104	2 PH1665	Ig heavy chain V r
24	392	58.2	119	2 PH0961	Ig heavy chain V r
25	390.5	57.9	120	2 S13999	Ig heavy chain V r
26	390	57.9	131	2 S26792	Ig heavy chain V r
27	389.5	57.8	122	2 PH0958	Ig heavy chain V r
28	389.5	57.8	128	2 PH0952	Ig heavy chain V r
29	386.5	57.3	135	2 B32274	Ig heavy chain pre

30	386	57.3	142	2 A32483	Ig heavy chain V r
31	386	57.3	160	2 PH0105	anti-PR2 erythrocy
32	385.5	57.3	136	2 PH0960	Ig heavy chain V r
33	385	57.1	126	2 S44151	Ig heavy chain V r
34	383.5	56.9	118	2 S38717	Ig heavy chain V r
35	383	56.8	125	2 PH0957	Ig heavy chain V r
36	383	56.8	125	2 S68170	Ig heavy chain V r
37	382.5	56.8	122	2 PH0887	Ig heavy chain V r
38	382	56.7	122	2 B49590	Ig heavy chain V r
39	381	56.5	117	2 S18552	Ig heavy chain V r
40	381	56.5	121	2 S20783	Ig heavy chain V r
41	378	56.1	98	2 S26919	Ig heavy chain V r
42	378	56.1	109	2 PH1668	Ig heavy chain V r
43	378	56.1	135	2 PH0953	Ig heavy chain V r
44	376.5	55.9	131	2 S66537	Ig heavy chain V r
45	374.5	55.6	110	2 PH1670	Ig heavy chain V r
46	374.5	55.6	116	2 PH0959	Ig heavy chain V r
47	374.5	55.6	116	2 S36261	Ig heavy chain V r
48	373	55.3	123	2 B30560	Ig heavy chain V r
49	372.5	55.3	139	2 A27609	Ig heavy chain pre
50	371	55.0	98	2 S26938	Ig heavy chain V r
51	371	55.0	117	2 S18551	Ig heavy chain V r
52	370.5	55.0	120	2 PH0962	Ig heavy chain V r
53	370	54.9	122	2 C49590	Ig heavy chain V r
54	370	54.9	246	2 S38950	Ig gamma-2a chain
55	370	54.9	446	2 S40295	Ig heavy chain V r
56	369.5	54.8	120	2 G28195	Ig heavy chain V r
57	368.5	54.7	110	2 PH1669	Ig heavy chain V r
58	368.5	54.7	128	2 C37267	Ig heavy chain V r
59	368	54.6	98	2 S26921	Ig heavy chain V r
60	368	54.6	117	2 S31680	Ig heavy chain V r
61	367	54.5	129	2 A33548	Ig heavy chain V-1
62	367	54.5	131	2 S21924	Ig heavy chain V r
63	366.5	54.4	117	2 S25176	Ig heavy chain V r
64	366.5	54.4	132	2 S31596	Ig heavy chain V r
65	365.5	54.2	120	2 F28195	Ig heavy chain V r
66	365	54.2	104	2 S69899	Ig heavy chain V r
67	364.5	54.1	128	2 A37267	Ig heavy chain V r
68	364	54.0	136	2 S04576	Ig heavy chain pre
69	363.5	53.9	241	2 S69131	Ig heavy chain (DO
70	363	53.9	98	2 S26912	Ig heavy chain V r
71	362.5	53.8	139	2 PS0024	Ig heavy chain pre
72	361.5	53.6	128	2 S37267	Ig heavy chain V r
73	361	53.6	98	2 S26920	Ig heavy chain V r
74	361	53.6	116	2 S31667	Ig heavy chain V r
75	361	53.6	117	1 HVHUGS	Ig heavy chain pre
76	360	53.4	98	2 S26918	Ig heavy chain V r
77	359	53.3	116	2 S24289	Ig gamma chain V r
78	359	53.3	117	2 PT0371	Ig gamma chain pre
79	359	53.3	121	2 H37266	Ig heavy chain V r
80	358.5	53.2	147	2 PH1561	Ig heavy chain V r
81	357	53.0	98	2 PH0871	Ig heavy chain V r
82	357	53.0	118	2 S38565	Ig heavy chain V r
83	357	53.0	140	2 PH1482	Ig heavy chain V r
84	356.5	52.9	117	2 B27563	Ig heavy chain V r
85	356	52.8	119	2 PH0089	Ig heavy chain V r
86	356	52.8	121	2 F37266	Ig heavy chain V r
87	355	52.7	111	2 PH0993	Ig heavy chain V r
88	355	52.7	113	2 PH1663	Ig heavy chain V r
89	355	52.7	125	2 S20639	Ig heavy chain V r
90	355	52.7	142	2 S19245	Ig heavy chain pre
91	354.5	52.6	119	2 F49590	Ig heavy chain V r
92	354	52.5	111	2 PH0932	Ig heavy chain V r
93	353	52.4	117	2 MHMS4E	Ig heavy chain V r
94	353	52.4	140	2 T01407	Ig heavy chain (my
95	352.5	52.3	119	2 JN0295	Ig heavy chain V-D
96	352.5	52.3	134	2 PH1422	Ig heavy chain V r
97	352	52.2	120	2 S03471	Ig heavy chain V-D
98	351.5	52.2	115	2 A54378	Ig heavy chain V r
99	351.5	52.2	120	2 S26789	Ig heavy chain V r
100	351	52.1	117	1 HVHUS5	Ig heavy chain pre

ALIGNMENTS

RESULT 1

S36260
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36260
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36260
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-129 <GRI>
A:Cross-references: EMBL:Z18851; NID:933124; PIDN:CAA79303.1; PID:9939903
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.28; Score 453; DB 2; Length 129;
Best Local Similarity 70.6%; Pred. No. 6.8e-36;
Matches 89; Conservative 9; Mismatches 26; Indels 2; Gaps 1;
QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 60
DB 4 LQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 63
QY 61 FQDVTFTADTSANTAYMELSLRSADTAVYICAR--VGPYSWDDSPQDNYNDVWGKGT 118
DB 64 LQGVNMTDTSTAYMELSLRSDDTAVYICARDFGYSCTSCPYYYNDVWGKGT 123
QY 119 TVIVSS 124
DB 124 TVIVSS 129

RESULT 2

S46393
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FIG>
A:Cross-references: EMBL:Z11680; NID:9509786; PIDN:CAA83485.1; PID:gl335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 56.68; Score 449; DB 2; Length 129;
Best Local Similarity 59.0%; Pred. No. 1.6e-35;
Matches 87; Conservative 9; Mismatches 28; Indels 2; Gaps 1;
QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 60
DB 4 LVQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 63
QY 61 FQDVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSP--QDNYNDVWGKGT 118
DB 64 FQGVNMTDTSTAYMELSLRSDDTAVYICARDFGYSCTSCPYYYNDVWGKGT 123
QY 119 TVIVSS 124
DB 124 TVIVSS 129

RESULT 3

PH1666
Ig heavy chain V region (clone 6C9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1666
R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylococcal protein A.
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1666
A:Molecule type: mRNA
A:Residues: 1-118 <HIL>
A:Experimental source: B cell
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 64.3%; Score 433.5; DB 2; Length 118;
Best Local Similarity 70.2%; Pred. No. 4.3e-34;
Matches 85; Conservative 12; Mismatches 19; Indels 5; Gaps 2;
QY 6 AEVKKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 65
DB 1 AEVKKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 60
QY 66 TPTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYNDVWGKGT 123
DB 61 TITRDTASATYMELSLRSDDTAVYICARV---TLGGIKFYFYGGVMDVWGKGT 117
QY 124 S 124
DB 118 S 118

RESULT 4

S19665
Ig heavy chain V region (alpha-phOx15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C:Accession: S19665; S24442
R:Mark, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 591-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19665
A:Molecule type: mRNA
A:Residues: 1-124 <MAR>
A:Cross-references: EMBL:X61647
R:Jones, P.T.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24442
A:Accession: S24442
A:Molecule type: mRNA
A:Residues: 1-40, 'GLSGDGSALTMVTSILDK', 61-118, 'T', 120-124 <JON>
A:Cross-references: EMBL:X61647; NID:937667; PIDN:CAA43828.1; PID:gl335368
A:Note: the difference for residues 41-60 results from misplacement of 10 bases in the staphylococcal protein A.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.2%; Score 432.5; DB 2; Length 124;
Best Local Similarity 67.7%; Pred. No. 5.7e-34;
Matches 84; Conservative 13; Mismatches 24; Indels 3; Gaps 1;
QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 60
DB 4 LVQSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGNIPYNGNKEFSK 63
QY 61 FQDVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYNDVWGKGT 120

```
Db 64 LQGRVTMTDTSTSTAYMELSLRSDDTAVYVCVRLLP---KRTATLHYIYDVMGKGLTV 120
QY 121 IVSS 124
    |||
Db 121 TVSS 124

RESULT 5
PH1667
IG heavy chain V region (clone 2H7) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1667
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1667
A:Molecule type: mRNA
A:Residues: 1-114 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 62.8%; Score 423.5; DB 2; Length 114;
Best Local Similarity 68.3%; Pred. No. 3.7e-33;
Matches 82; Conservative 12; Mismatches 19; Indels 7; Gaps 3;

QY 6 AEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMWNPYNGNKEFSKAFQDRV 65
    |||
Db 1 AEVKKPGASVKVSCASGYTFTSYAHWRQAPGQRLWNGWLNAGNGNTKYAQKFGSRV 60

QY 66 TPTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYI-MDVWGKGLTVVSS 124
    |||
Db 61 TITRDTASATAYMELSLRSSEDTAVYICARVYDF-W-----SGYAFDIWGQGTMTVSS 114

RESULT 6
S29257
IG heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouhane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A:Title: Molecular characterization of a human anti-Bh(D) antibody with a D(H) segment
A:Reference number: S29257; MUID:92382614; PMID:1499555
A:Accession: S29257
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:S42403; NID:9253699; PIDN:AAB22940.1; PID:9253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.2%; Score 419; DB 2; Length 148;
Best Local Similarity 62.7%; Pred. No. 1.3e-32;
Matches 84; Conservative 11; Mismatches 21; Indels 18; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMWNPYNGNKEFSK 60
    |||
Db 23 LVQSGAEVKKPGASVKVSCASGYTFTFYAHWRQAPGQSLWNGWISVADGKTKYSQK 82

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQD-----Y 110
    |||
Db 83 FQDRVTITRDTSATAYMEVRLSRSEDTAVYICAR-----SPRINNVRLVITTPPW 134

QY 111 MDVWGKGLTVVSS 124
    |||
Db 135 FDSWGQGLTVVSS 148
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RESULT 7
D33548
IG heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression in B cell precursors
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: D33548
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.9%; Score 417; DB 2; Length 123;
Best Local Similarity 65.3%; Pred. No. 1.7e-32;
Matches 81; Conservative 9; Mismatches 30; Indels 4; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMWNPYNGNKEFSK 60
    |||
Db 4 LVQSGAEVKKPGASVKVSCASGYTFTGHYHWRQAPGQGLEWNGWLNPNSGGTNYAEK 63

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYIYDVWGKGLTV 120
    |||
Db 64 FQGRVTITRDTSTANTAYMELSLRSDDTAVYICARASYCYGD-----CYFFDYWGQGLTV 119

QY 121 IVSS 124
    |||
Db 120 TVSS 123

RESULT 8
S36265
IG heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36265
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>
A:Cross-references: EMBL:Z18846; NID:9313121; PIDN:CAA79298.1; PID:9939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 416.5; DB 2; Length 118;
Best Local Similarity 65.1%; Pred. No. 1.8e-32;
Matches 82; Conservative 11; Mismatches 20; Indels 13; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFPEWGMWNPYNGNKEFSK 60
    |||
Db 4 LVQSGAEVKKPGASVKVSCASGYTFTGYHWRQAPGQGLEWNGWLNPNSGGTNYAQK 63

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQD--NTYMDVWGKGT 118
    |||
Db 64 FQGRVTITRDTSTANTAYMELSLRSSEDTAVYICAR-----DPLSGYLDVWGQGT 112

QY 119 TVVSS 124
    |||
Db 113 LTVSS 118

RESULT 9
C33548
```

Ig heavy chain V-1 region (783) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: C33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-133 <KIP>
A:Experimental source: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
Query Match 61.3%; Score 413; DB 2; Length 133;
Best Local Similarity 65.4%; Pred. No. 4.3e-32; Indels 2;
Matches 85; Conservative 11; Mismatches 28; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 4 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 63
QY 61 FQGRVTITADTSANTAYMELSLRSADTAVYCAR---VGPYSWDDSPQDNY---MDVW 114
Db 64 FQGRVTITADTSANTAYMELSLRSADTAVYCAR---VGPYSWDDSPQDNY---MDVW 123
QY 115 GKGTIVVSS 124
Db 124 GQGTIVVSS 133
RESULT 10
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FRI>
A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 61.3%; Score 413; DB 2; Length 627;
Best Local Similarity 65.4%; Pred. No. 2.2e-31; Indels 6; Gaps 2;
Matches 85; Conservative 11; Mismatches 28; Indels 6; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 82
QY 61 FQGRVTITADTSANTAYMELSLRSADTAVYCAR---VGPYSWDDSPQDNY---MDVW 114
Db 83 FQGRVTITADTSANTAYMELSLRSADTAVYCAR---VGPYSWDDSPQDNY---MDVW 142
QY 115 GKGTIVVSS 124
Db 143 GQGTIVVSS 152
RESULT 11
PH0955

Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0955
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0955
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-127 <MA3>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-115/Region: complementarity-determining 3
Query Match 60.5%; Score 408; DB 2; Length 127;
Best Local Similarity 66.9%; Pred. No. 1.2e-31; Indels 0; Gaps 0;
Matches 83; Conservative 8; Mismatches 33; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 4 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 63
QY 61 FQGRVTITADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 64 FQGRVTITADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 123
QY 121 IVSS 124
Db 124 TVSS 127
RESULT 12
S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
Query Match 59.7%; Score 402.5; DB 2; Length 136;
Best Local Similarity 63.7%; Pred. No. 4.3e-31; Indels 11; Gaps 2;
Matches 79; Conservative 14; Mismatches 20; Indels 11; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 23 LVQSGAEVKKPGASVKVSCASGYTFTSYDINWVRAQPGQRFEMWGWINPYNGNKEFSK 82
QY 61 FQGRVTITADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 83 FQGRVTITADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 131
QY 121 IVSS 124
Db 132 TVSS 135

RESULT 13

ELHUND
 Ig heavy chain precursor V-I region (Nd) - human (fragments)
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
 C:Accession: A93933; A02026
 R:Kanten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
 A>Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
 A:Reference number: A93933; MUID:83065234; PMID:6815656
 A:Accession: A93933
 A:Molecule type: mRNA
 A:Residues: 1-143 <KEN>
 R:Bannich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
 in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
 A:Reference number: A94418
 A:Contents: annotation; partial sequence
 A>Note: this epsilon chain was isolated from a myeloma protein
 C:Genetics:
 A:Gene: GDB:IGHV@
 A:Cross-references: GDB:128528; OMIM:147070
 A:Map Position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
 F:30-113/Domain: immunoglobulin homology <IMM>
 F:16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
 F:37-111/Disulfide bonds: #status experimental

Query Match 59.7%; Score 402.5; DB 1; Length 143;
 Best Local Similarity 60.3%; Pred. No. 4.6e-31;
 Matches 76; Conservative 20; Mismatches 27; Indels 3; Gaps 2;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQGRFEMWGWINPYNGNKEFSK 60
 DB 19 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQGRFEMWGWINPYNGNKEFSK 60
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVPYSWDD--SPQDNYMDVWGKCT 118
 DB 79 FQGRVTWTRDASTAYMDLSRLSRSDSAVFYCAKSDPP-WSDDYNYFDYSYILDVWGQGT 137
 QY 119 TVIVSS 124
 DB 138 TTVVSS 143

RESULT 14

S36271
 Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMOB J. 12, 725-734, 1993
 A>Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S36256; MUID:93178448; PMID:7679990
 A:Accession: S36271
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-122 <GRI>
 A:Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
 F:30-113/Domain: immunoglobulin homology <IMM>

Query Match 59.3%; Score 400; DB 2; Length 122;
 Best Local Similarity 63.7%; Pred. No. 6.6e-31;
 Matches 79; Conservative 11; Mismatches 24; Indels 10; Gaps 3;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQGRFEMWGWINPYNGNKEFSK 60

Db 4 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQGRFEMWGWINPYNGNKEFSK 63
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVPYSWDDSPQDNYMDVWGK 116
 Db 64 LQGRVTWTRDASTAYMDLSRLSRSDSAVFYCAKSDPP-WSDDYNYFDYSYILDVWGQ 117
 QY 117 GTTV 120
 Db 118 GTIV 121

RESULT 15

S46394
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S46394
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 J. Mol. Biol. 239, 68-78, 1994
 A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
 A:Reference number: S46390; MUID:94254092; PMID:8196048
 A:Accession: S46394
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-132 <FIG>
 A:Cross-references: EMBL:Z31681; NID:g509788; PIDN:CAA83486.1; PID:gl3335147
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.1%; Score 398.5; DB 2; Length 132;
 Best Local Similarity 64.1%; Pred. No. 1e-30;
 Matches 84; Conservative 6; Mismatches 32; Indels 9; Gaps 2;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQGRFEMWGWINPYNGNKEFSK 60
 Db 4 LVQSGAEVKKPGSSVKVSKASGGTFSYALSWVRQAPQGRFEMWGWIPIFGTANHAQ 63
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCAR-----VGPYSWDDSPQDNYMDV 113
 Db 64 FQGRVTWTRDASTAYMDLSRLSRSDSAVFYCAKSDPP-PAADTGILEW--LPSYYYNDV 121
 QY 114 WGKGTIVVSS 124
 Db 122 WGKGTIVTVSS 132

RESULT 16

S18553
 Ig heavy chain V region precursor (VI-3b) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
 C:Accession: S18553; S26916
 R:Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc
 EMOB J. 10, 3641-3645, 1991
 A>Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
 A:Reference number: S18551; MUID:92037524; PMID:1935893
 A:Accession: S18553
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-117 <SHI>
 A:Cross-references: EMBL:X62109
 R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A>Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v.
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26916
 A:Molecule type: DNA
 A:Residues: 20-117 <TOM>
 A:Cross-references: EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID:g32872
 C:Genetics:
 A:Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 397; DB 2; Length 117;
Best Local Similarity 77.9%; Pred. No. 1.2e-30;
Matches 74; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFVWGWINPYNKKEFSK 60
DB 23 LVQSGAEVKKPGSSVKVSKASGGTFSYALSWVRQAPGQGLEWMGGIIPIFGTANYAQK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCAR 95
DB 83 FQGRVTITRTDSASTAYMELSLRSADTAVYYCAR 117

RESULT 17
S34014
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34014; S30535
R;Marti, X.; Tsapis, A.; Brouet, J.C.
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34014
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:Z18321
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 58.8%; Score 396; DB 2; Length 127;
Best Local Similarity 60.3%; Pred. No. 1.7e-30;
Matches 79; Conservative 15; Mismatches 19; Indels 18; Gaps 2;

QY 3 QSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFVWGWINPYNKKEFSK 62
DB 6 QSGAEVKKPGASVKVSKASGGTFSYALSWVRQAPGQGLEWMGGIIPFGTANYAQK 65
QY 63 DRVTFTADTSANTAYMELSLRSADTAVYYCARV-----GPSWDDSPQNTYMDV 113
DB 66 GRVTMTNTSTAYMELSLRSADTAVYYCARLSIGAVIRGY-----YALDV 116

QY 114 WGKGTIVVSS 124
DB 117 WGQGTIVSVSS 127

RESULT 18
B33548
Ig heavy chain V-1 region (AND) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: B33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: B33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-126 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 395.5; DB 2; Length 126;
Best Local Similarity 63.8%; Pred. No. 1.8e-30;
Matches 83; Conservative 8; Mismatches 26; Indels 13; Gaps 2;

QY 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFVWGWINPYNKKEFSK 60
DB 4 LVQSGAEVKKPGSSVKVSKASGGTFSYALSWVRQAPGQGLEWMGGIIPIFGTANYAQK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARV-----PYSWDDSPQNTYMDV 114
DB 64 FQGRVTITADESTAYMELSLRSADTAVYYCARVSIKGVQHY--Y--YMDV 116

QY 115 GKGTIVVSS 124
DB 117 GLGTIVTVSS 126

RESULT 19
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

Query Match 58.7%; Score 395.5; DB 2; Length 132;
Best Local Similarity 63.4%; Pred. No. 1.9e-30;
Matches 83; Conservative 10; Mismatches 29; Indels 9; Gaps 2;

QY 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFVWGWINPYNKKEFSK 60
DB 4 LVQSGAEVKKPGSSVKVSKASGGTFSYALSWVRQAPGQGLEWMGGIIPFGTANYAQK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQNTY--MDV 113
DB 64 FQGRVTITADESTAYMELSLRSADTAVYYCAR--PHASIDDFWGYPNYYGMDV 121

QY 114 WGKGTIVVSS 124
DB 122 WGQGTIVTVSS 132

RESULT 20
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>

A;Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID:G560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 395.5; DB 2; Length 135;
Best Local Similarity 62.9%; Pred. No. 2e-30;
Matches 78; Conservative 11; Mismatches 24; Indels 11; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQASGVRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
DB 23 LVQSGAEVKKPGASVKVSQASGVRFTFTGYYTHWVROAPGQGLEWMMGWINPNSGGTNYAQK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQGRVTMTDTSISTAYMELSLRSDTAVYCARA-----RTGY--NYWGQGTIV 131
QY 121 IVSS 124
DB 132 TVSS 135

RESULT 21

A49590
Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
C;Accession: A49590
R;Burioni, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.; Burton, D.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 355-359, 1994
A;Title: Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents cell death
A;Reference number: A49590; MUID:94105188; PMID:8278393
A;Accession: A49590
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-121 <BUT>
A;Experimental source: bone marrow lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBI:141850)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 58.5%; Score 394; DB 2; Length 121;
Best Local Similarity 66.4%; Pred. No. 2.4e-30;
Matches 81; Conservative 10; Mismatches 29; Indels 2; Gaps 1;
QY 3 QSGAEVKKPGASVKVSQASGVRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 62
DB 2 ESGAEVKKPGSSVKVSCKTSGGAFSSYAINWVROAPGQGLEWVGGLPVFGTNEAQK 61
QY 63 DRYVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 122
DB 62 GRVTFADASTTAYMELSLRSDTAVYCARVGYCSTNGCSLGG--MDVWGQGTIV 119
QY 123 SS 124
DB 120 SS 121

RESULT 22

S23623
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23623
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from B cells
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23623
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <OLE>
A;Cross-references: EMBL:X59702; NID:G32010; PIDN:CAA42223.1; PID:G32011

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 393.5; DB 2; Length 171;
Best Local Similarity 63.0%; Pred. No. 3.9e-30;
Matches 80; Conservative 11; Mismatches 29; Indels 7; Gaps 3;
QY 1 LEQSGAEVKKPGASVKVSQASGVRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
DB 23 LVQSGAEVKKPGASVKVSCKGSGYFTTAYQMHVROAPGQGLEWMMGWINPNSGGTGYGQK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 117
DB 83 FQGRVTMTDTSISTAYMELSLRSDTAVYCARI--EYFDGSLKPSDV--DINGQG 138
QY 118 TTVIVSS 124
DB 139 TMTVTSS 145

RESULT 23

PH1665
Ig heavy chain V region (clone 6B8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1665
R;Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315389
A;Accession: PH1665
A;Molecule type: mRNA
A;Residues: 1-104 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 392.5; DB 2; Length 104;
Best Local Similarity 64.7%; Pred. No. 2.9e-30;
Matches 77; Conservative 10; Mismatches 17; Indels 15; Gaps 1;
QY 6 AEVKKPGASVKVSQASGVRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 65
DB 1 AEVKKPGASVKVSCKASGYFTSYAMHWVROAPGQRLWMMGGINAGNGNTKYAQK 60
QY 66 TFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 124
DB 61 TITRDTASTAYMELSLRSDTAVYCAR-----EDYWGQGTIV 104

RESULT 24

PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-119 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2

F:15-98/Region: framework 3	
F:99-107/Region: complementarity-determining 3	
Query Match	58.2%; Score 392; DB 2; Length 119;
Best Local Similarity	66.1%; Pred. No. 3.7e-30;
Matches	82; Conservative 9; Mismatches 25; Indels 8; Gaps 2;
QY	1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPQGFQFWMGWINPYNGNKFSK 60
DB	4 LVQSGAEVKPGASVKVSCKASGTYFTSYAIVSWVRQAPQGLEWVGIIPIFGTANYAQK 63
QY	61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
DB	64 FQGRVTITADESTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 115
QY	121 IVSS 124
DB	116 TVSS 119
RESULT 25	
S31999	
Ig heavy chain V region - human (fragment)	
C:Species: Homo sapiens (man)	
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999	
C:Accession: S31999	
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.	
submitted to the EMBL Data Library, June 1992	
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as	
A:Reference number: S31977	
A:Accession: S31999	
A:Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-120 <P>	
A:Cross-references: EMBL:Z15084; NID:G38507; PIDN:CAA78793.1; PID:G38508	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:15-98/Domain: immunoglobulin homology <IMM>	
Query Match	57.9%; Score 390.5; DB 2; Length 120;
Best Local Similarity	60.0%; Pred. No. 5.2e-30;
Matches	75; Conservative 16; Mismatches 25; Indels 9; Gaps 2;
QY	1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPQGFQFWMGWINPYNGNKFSK 60
DB	4 LLESGAEVKPGASVKVSCKASGTYFTSYAIVSWVRQAPQGLEWVGIIPIFGTANYAQK 63
QY	61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTT 119
DB	64 FQGRVTITADESTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTT 115
QY	120 IVSS 124
DB	116 TVSS 120
RESULT 26	
S26792	
Ig heavy chain V region - human	
C:Species: Homo sapiens (man)	
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000	
C:Accession: S26792	
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.	
Eur. J. Immunol. 22, 241-245, 1992	
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami	
A:Reference number: S26786; MUID:92111632; PMID:11730251	
A:Accession: S26792	
A:Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-131 <MOR>	
A:Cross-references: EMBL:X61012; NID:G32804; PIDN:CAA43346.1; PID:G1335131	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:15-98/Domain: immunoglobulin homology <IMM>	
Query Match	57.8%; Score 389.5; DB 2; Length 122;
Best Local Similarity	63.8%; Pred. No. 6.5e-30;
Matches	81; Conservative 10; Mismatches 25; Indels 11; Gaps 2;
QY	1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPQGFQFWMGWINPYNGNKFSK 60
DB	4 LVQSGAEVKPGASVKVSCKASGTYFTSYAIVSWVRQAPQGLEWVGIIPIFGTANYAQK 63
QY	61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGK 117
DB	64 FQGRVTITADESTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGK 115
QY	118 TVIVSS 124
DB	116 TVTVSS 122
RESULT 28	
PH0952	
Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)	
C:Species: Homo sapiens (man)	
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996	
C:Accession: PH0952	
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.	
J. Exp. Med. 175, 983-991, 1992	
A:Title: Evidence for somatic selection of natural autoantibodies.	
A:Reference number: PH0952; MUID:92202880; PMID:1552291	
A:Accession: PH0952	
A:Status: nucleic acid sequence not shown	
A:Molecule type: DNA	
F:15-98/Domain: immunoglobulin homology <IMM>	
Query Match	57.9%; Score 390; DB 2; Length 131;
Best Local Similarity	59.4%; Pred. No. 6.3e-30;
Matches	76; Conservative 18; Mismatches 30; Indels 4; Gaps 2;
QY	1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPQGFQFWMGWINPYNGNKFSK 60
DB	4 LVQSGAEVKPGASVKVSCKASGTYFTSYAIVSWVRQAPQGLEWVGIIPIFGTANYAQK 63
QY	61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGK 116
DB	64 FTGRFVSLDTSTAYLQISLKAEATVYICARVGPYSWDDSPQDNYMDVWGK 123
QY	117 GTTVIVSS 124
DB	124 GTTVTVSS 131
RESULT 27	
PH0958	
Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)	
C:Species: Homo sapiens (man)	
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996	
C:Accession: PH0958	
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.	
J. Exp. Med. 175, 983-991, 1992	
A:Title: Evidence for somatic selection of natural autoantibodies.	
A:Reference number: PH0952; MUID:92202880; PMID:1552291	
A:Accession: PH0958	
A:Status: nucleic acid sequence not shown	
A:Molecule type: DNA	
A:Residues: 1-122 <MAR>	
C:Superfamily: immunoglobulin V region; immunoglobulin homology	
C:Keywords: heterotetramer; immunoglobulin	
F:1-30/Region: framework 1	
F:15-98/Domain: immunoglobulin homology <IMM>	
F:31-35/Region: complementarity-determining 1	
F:36-50/Region: framework 2	
F:51-67/Region: complementarity-determining 2	
F:68-98/Region: framework 3	
F:99-110/Region: complementarity-determining 3	

A;Residues: 1-128 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-116/Region: complementarity-determining 3

Query Match 57.8%; Score 389.5; DB 2; Length 128;
Best Local Similarity 64.3%; Pred. No. 6.9e-30;
Matches 81; Conservative 10; Mismatches 32; Indels 3; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMMGWNPYNGNKEFSAK 60
DB 4 LVQSGAEVKPGSVKVCASGGTFSYAIWVROAPGQGLEWGGIPIFTANYAQK 63

QY 61 FQDRVTFTADTSANTAYMELRSADTAVYCARVGPYS--WDDSPQDNYMDVWGKGT 118
DB 64 FQGRVTITADKSTSTAYMELSLRSEDATVYVCARGGNVDYIW-GSYRSNDAPDIWGQST 122

QY 119 TVIVSS 124
DB 123 MVTVSS 128

RESULT 29
B32274
Ig heavy chain precursor V-I region (EVI-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Oct-1996
C;Accession: B32274
R;Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1518, 1988
A;Title: Complete protein sequences of the variable regions of the cloned heavy and light
actors of the Wa idiotype family
A;Reference number: A92767; MUID:88213701; PMID:2452836
A;Accession: B32274
A;Molecule type: DNA
A;Residues: 1-135 <NEW>
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;4-135/Product: Ig heavy chain V-I region EVI-15 #status predicted <HVI>
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 57.3%; Score 386.5; DB 2; Length 135;
Best Local Similarity 60.7%; Pred. No. 1.4e-29;
Matches 82; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMMGWNPYNGNKEFSAK 60
DB 7 LVQSGAEVKPGSVKVCASGGTFSYAFWVROAPGQGLEWGGIIPFLGTHYAK 66

QY 61 FQDRVTFTADTSANTAYMELRSADTAVYCARVGPYSWDDSDS-----POD-NYV-- 110
DB 67 FQGRVTITDBSTRTAYMELHILRSEDATVYCAR-----DOSLENIEVPLDPNIFYD 120

QY 111 -MDVWGKGTIVVSS 124
DB 121 GMDVWGQGTIVTVSS 135

RESULT 30
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, O

Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usir
A;Reference number: A32483; MUID:89273586; PMID:2499327
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

Query Match 57.3%; Score 386; DB 2; Length 142;
Best Local Similarity 57.7%; Pred. No. 1.6e-29;
Matches 79; Conservative 9; Mismatches 23; Indels 26; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMMGWNPYNGNKEFSAK 60
DB 14 LVQSGAEVKPGASVKVSCASGYTFINYYHWVROAPGQGLEWNGIINPSGNSTNYAQK 73

QY 61 FQDRVTFTADTSANTAYMELRSADTAVYCAR-----VGPSWDDSDSPQD 107
DB 74 FQGRVTITRDTSTSTVYMELSLRSEDATVYVCAREKLATTIFGVLIITG----- 123

QY 108 NYMDVWGKGTIVVSS 124
DB 124 ---MDYWGQGTIVTVSS 137

Search completed: August 26, 2004, 13:39:51
Job time : 13.9407 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:27 ; Search time 7.34815 seconds
(without alignments)
878.684 Million cell updates/sec

Title: US-10-016-986-66

Perfect score: 674

Sequence: 1 LEQSGAEVKKPGASVKVSQ.....PDNYYMDVWGKTTIVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402.5	59.7	147	1	HVIC HUMAN
2	363.5	53.9	120	1	HV1H HUMAN
3	361	53.6	117	1	HV1B HUMAN
4	357	53.0	120	1	HV03 MOUSE
5	353	52.4	117	1	HV12 MOUSE
6	351	52.1	117	1	HV1G HUMAN
7	348	51.6	117	1	HV13 MOUSE
8	344.5	51.1	118	1	HV51 MOUSE
9	342.5	50.8	139	1	HV07 MOUSE
10	339.5	50.4	120	1	HV50 MOUSE
11	339.5	50.3	140	1	HV02 MOUSE
12	325.5	48.3	137	1	HV11 MOUSE
13	324	48.1	138	1	HV48 MOUSE
14	321.5	47.7	114	1	HV00 MOUSE
15	321	47.6	117	1	HV1A HUMAN
16	319	47.3	125	1	HV1F HUMAN
17	318	47.2	121	1	HV01 MOUSE
18	315	46.7	117	1	HV14 MOUSE
19	310	46.0	136	1	HV15 MOUSE
20	309	45.8	117	1	HV09 MOUSE
21	307	45.5	117	1	HV04 MOUSE
22	303	45.0	117	1	HV52 MOUSE
23	300.5	44.6	119	1	HV38 MOUSE
24	297	44.1	117	1	HV06 MOUSE
25	292	43.3	117	1	HV49 MOUSE
26	287	42.6	117	1	HV10 MOUSE
27	286	42.4	117	1	HV05 MOUSE
28	285.5	42.4	136	1	HV16 MOUSE
29	279.5	41.5	122	1	HV3G HUMAN
30	278.5	41.3	124	1	HV1E HUMAN
31	276.5	41.0	122	1	HV20 MOUSE
32	276	40.9	123	1	HV25 MOUSE
33	275	40.8	121	1	HV3J HUMAN

ALIGNMENTS

RESULT 1

34	275	40.8	123	1	HV22_MOUSE
35	273.5	40.6	122	1	HV21_MOUSE
36	273.5	40.6	124	1	HV1D_HUMAN
37	272.5	40.4	122	1	HV3H_HUMAN
38	272	40.4	118	1	HV39_MOUSE
39	272	40.4	119	1	HV3I_HUMAN
40	272	40.4	123	1	HV19_MOUSE
41	271.5	40.3	119	1	HV37_MOUSE
42	271	40.2	123	1	HV18_MOUSE
43	270	40.1	123	1	HV23_MOUSE
44	270	40.1	123	1	HV24_MOUSE
45	268.5	39.8	119	1	HV40_MOUSE
46	266.5	39.5	146	1	HV2I_HUMAN
47	265	38.3	117	1	HV42_MOUSE
48	264	39.2	144	1	HV26_MOUSE
49	261	38.7	117	1	HV41_MOUSE
50	260.5	38.6	119	1	HV3P_HUMAN
51	260	38.6	115	1	HV3D_HUMAN
52	256	38.0	137	1	HV46_MOUSE
53	255.5	37.9	126	1	HV3K_HUMAN
54	253.5	37.6	122	1	HV3A_HUMAN
55	250	37.1	144	1	HV43_MOUSE
56	249	36.9	142	1	HV01_RAT
57	243.5	36.1	116	1	HV3T_HUMAN
58	242.5	36.0	120	1	HV3U_HUMAN
59	242	35.9	120	1	HV3E_HUMAN
60	241	35.8	119	1	HV3L_HUMAN
61	240.5	35.7	115	1	HV3S_HUMAN
62	240	35.6	116	1	HV36_MOUSE
63	240	35.6	117	1	HV2G_HUMAN
64	239	35.5	116	1	HV3R_HUMAN
65	238.5	35.4	117	1	HV3O_HUMAN
66	238	35.3	115	1	HV3F_HUMAN
67	237.5	35.2	111	1	HV35_MOUSE
68	237.5	35.2	118	1	HV3V_HUMAN
69	237	35.2	129	1	HV2F_HUMAN
70	236.5	35.1	114	1	HV3B_HUMAN
71	236.5	35.1	119	1	HV3M_HUMAN
72	236	35.0	117	1	HV3C_HUMAN
73	235	34.9	117	1	HV55_MOUSE
74	234.5	34.8	119	1	HV3N_HUMAN
75	234.5	34.8	135	1	HV02_XENIA
76	232	34.4	116	1	HV61_MOUSE
77	231	34.3	116	1	HV3Q_HUMAN
78	231	34.3	117	1	HV17_MOUSE
79	230.5	34.2	114	1	HV01_CANFA
80	229	34.0	113	1	HV30_MOUSE
81	229	34.0	115	1	HV32_MOUSE
82	228	33.8	117	1	HV54_MOUSE
83	227	33.7	117	1	HV03_CARAU
84	225	33.4	115	1	HV33_MOUSE
85	224	33.2	113	1	HV27_MOUSE
86	224	33.2	117	1	HV01_CAICR
87	223.5	33.2	97	1	HV56_MOUSE
88	223	33.1	98	1	HV57_MOUSE
89	223	33.1	113	1	HV31_MOUSE
90	222	32.9	113	1	HV28_MOUSE
91	222	32.9	117	1	HV02_CANFA
92	219	32.5	113	1	HV34_MOUSE
93	219	32.5	116	1	HV60_MOUSE
94	217	32.2	117	1	HV03_CAICR
95	217	32.2	117	1	HV58_MOUSE
96	217	32.2	121	1	HV2E_HUMAN
97	215	31.9	113	1	HV29_MOUSE
98	215	31.8	117	1	HV53_MOUSE
99	214.5	31.8	116	1	HV05_CARAU
100	214.5	31.8	116	1	HV45_MOUSE

HVIC_HUMAN
ID HVIC_HUMAN STANDARD; PRT; 147 AA.
AC P01744; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83065234; PubMed=6815656;
RX Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.,
DE "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
[2]
SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.,
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT CHAIN 1
FT SIGNAL 19
FT CHAIN 20 147
FT DOMAIN 20 131
FT MOD_RES 20 20
FT PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21
FT CONFLICT 53 54
FT CONFLICT 67 68
FT CONFLICT 125 125
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 59.7%; Score 402.5; DB 1; Length 147;
Best Local Similarity 60.3%; Pred. No. 2.8e-35;
Matches 76; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

QY 1 LEQSGAEYKPGASVYSCASGYRFSNFIHWVRQAPGQRFEMGWINPYNGKFSK 60
DB 23 LVQSGAEYKPGASVYSCASGYRFSNFIHWVRQAPGQRFEMGWINPYNGKFSK 82
QY 61 FQDRVTFTADTSANTAYMEKLSRSADTAVYCARVGPYSWDD--SPQDNYVDVWGKT 118
DB 83 FQGRVTFTADTSANTAYMEKLSRSADTAVYCARVGPYSWDD--SPQDNYVDVWGKT 141
QY 119 TVIVSS 124
DB 142 TVIVSS 147

RESULT 2
HV1B_HUMAN
ID HV1B_HUMAN STANDARD; PRT; 120 AA.
AC P80421;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95255298; PubMed=7737190;
RX Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.,
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins."
Eur. J. Biochem. 228:886-893(1995).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW immunoglobulin V region.
FT DOMAIN 1 111
FT DISULFID 22 95
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;

Query Match 53.9%; Score 363.5; DB 1; Length 120;
Best Local Similarity 61.3%; Pred. No. 2.8e-31;
Matches 76; Conservative 13; Mismatches 28; Indels 7; Gaps 3;

QY 1 LEQSGAEYKPGASVYSCASGYRFSNFIHWVRQAPGQRFEMGWINPYNGKFSK 60
DB 4 LVQSGAEYKPGASVYSCASGYRFSNFIHWVRQAPGQRFEMGWINPYNGKFSK 62
QY 61 FQDRVTFTADTSANTAYMEKLSRSADTAVYCARVGPYSWDDSPQDNYVDVWGKT 120
DB 63 FQDRVTFTADTSANTAYMEKLSRSADTAVYCARVGPYSWDDSPQDNYVDVWGKT 116
QY 121 IVSS 124
DB 117 IVSS 120

RESULT 3
HV1B_HUMAN
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83144028; PubMed=6298778;
RX Rechavi G., Ram D., Glazer L., Zakut R., Givol D.,
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

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CC -----J00240; AAAS2988.1; -.
DR PIR; A02024; HVHUG.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1PE7 CRC64;

Query Match 53.6%; Score 361; DB 1; Length 117;
Best Local Similarity 71.6%; Pred. No. 4.9e-31;
Matches 68; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCKASQGVYFVHVRQAPGQRFQFWMGWINPYNGNKFSK 60
DB 23 LVQSGAEVKKPGASVKVSCKASGYTFNSYTHHVRQAPGQGLEWVGIINPSGGSTSYAQK 82
QY 61 FQDRVTFATDSANTAYMELSLRSADTAVYVCARVGPVSWDDSPQDNYNDVWGKGTTV 95
DB 83 FQGRVTMTDTSSTVYMWELSLRSADTAVYVCAR 117

RESULT 4
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8313846; PubMed=6186498;
RA Siekevitz M., Geiter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idio type response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybriidoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 53.0%; Score 357; DB 1; Length 120;
Best Local Similarity 53.2%; Pred. No. 1.3e-30;
Matches 66; Conservative 26; Mismatches 26; Indels 6; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSCKASQGVYFVHVRQAPGQRFQFWMGWINPYNGNKFSK 60

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DB 3 LQSGAEIVRAGSSVKMSCKASGYFTSYGINVWVQRPGQGLEWIGYINPGNGYTKYNEK 62
QY 61 FQDRVTFATDSANTAYMELSLRSADTAVYVCARVGPVSWDDSPQDNYNDVWGKGTTV 120
DB 63 FKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSVYIG-----GSYFYDWGCGTTL 116
QY 121 IVSS 124
DB 117 TVSS 120

RESULT 5
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC -!- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MHMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 52.4%; Score 353; DB 1; Length 117;
Best Local Similarity 54.0%; Pred. No. 3.4e-30;
Matches 67; Conservative 20; Mismatches 27; Indels 10; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCKASQGVYFVHVRQAPGQRFQFWMGWINPYNGNKFSK 60
DB 4 LQSGPELVKPGASVKMSCKASGYFTTDYMKVQSHGKSLWIGDINPNNGGTSYNQK 63
QY 61 FQDRVTFATDSANTAYMELSLRSADTAVYVCARVGPVSWDDSPQDNYNDVWGKGTTV 120
DB 64 FKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCAR--DYDW-----YFDVWGAGTTV 113
QY 121 IVSS 124
DB 114 TVSS 117

RESULT 6
HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296408; PubMed=2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
 RA Ohno K., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 RT heavy-chain locus";
 RL EMO J. 7:1047-1051(1988).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; X07448; -; NOT ANNOTATED_CDS.
 DR PIR; S00476; HVH035.
 DR HSSP; P01772; 2PB4
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW CHAIN 1 19 IG HEAVY CHAIN V-I REGION V35.
 FT SIGNAL 1 19 IG-
 FT DOMAIN 20 >117 IG-
 FT NON_TER 117
 FT SEQUENCE 117 AA; 13009 MW; BB61CE63F8CE97BD CRC64;
 SQ
 Query Match 52.1%; Score 351; DB 1; Length 117;
 Best Local Similarity 70.5%; Pred. No. 5.5e-30;
 Matches 67; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKGFSAK 60
 DB 23 LVQSGAEVKKPGASVKVSQASGYRFTGTYHWVRQAPGQGLEWNGRINPNSGTYAQK 82
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCAR 95
 DB 83 FQGRVTSTRTSISTAYMELSLRSDDTVVYVCAR 117
 RESULT 7
 HV13_MOUSE
 ID HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Cleveringer B., Davis J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments.";

RL Nature 283:35-40(1980).
 CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A26242; MHMSJ5.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 116 IG-LIKE.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 117
 FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
 SQ
 Query Match 51.6%; Score 348; DB 1; Length 117;
 Best Local Similarity 53.6%; Pred. No. 1.1e-29;
 Matches 67; Conservative 20; Mismatches 26; Indels 12; Gaps 2;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKGFSAK 60
 DB 4 LQSGPELVKPGASVKVSQASGYRFTDYMKWKQSHGKSLWIGDINPNNGTSTNQK 63
 QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNY-YMDVWGKGT 119
 DB 64 FQKATLVKSSSTAYMQLNLSLSESAVYVCAR-----DRYFYDVGAGTT 112
 QY 120 VIVSS 124
 DB 113 VTVSS 117
 RESULT 8
 HV51_MOUSE
 ID HV51_MOUSE STANDARD; PRT; 118 AA.
 AC P06330;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region AC38 205.12.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84182519; PubMed=6201362;
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes.";
 RL EMO J. 3:517-523(1984).
 DR PIR; A02040; MHMS38.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 99 104 D SEGMENT.
 FT DOMAIN 105 118 J SEGMENT.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 118
 FT SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
 SQ
 Query Match 51.1%; Score 344.5; DB 1; Length 118;
 Best Local Similarity 53.2%; Pred. No. 2.7e-29;
 Matches 66; Conservative 21; Mismatches 28; Indels 9; Gaps 2;


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OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
CX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=62152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00493; AAA38128.1; -.
CC PIR; A94264; HVMSG7.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Hybridoma; Signal.
CC SIGNAL 1 19
CC CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
CC DOMAIN 20 139 IG-LIKE.
CC NON TER 140 140
CC SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 50.3%; Score 339; DB 1; Length 140;
Best Local Similarity 51.6%; Pred. No. 1.2e-28;
Matches 64; Conservative 25; Mismatches 29; Indels 6; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGRFNFVHVRQAPGQRFWMGWINPYNKPEFSK 60
DB 23 LQSGAEVKKPGASVKVSQASGRFNFVHVRQAPGQRFWMGWINPYNKPEFSK 82
QY 61 FQDRVTFTADTSANTAYNELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FRGKTTLVTKSSSTAYNQLSLTSSEDSAVYFCARSHYIG-----GSDYFDYWGQGTPL 136
QY 121 IVSS 124
DB 137 TVSS 140

RESULT 12
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
CX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=61234546; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Keth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of

Mus musculus (Mouse)
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981)
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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CC -----
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 122 D SEGMENT.
CC DOMAIN 123 137 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 137 137
CC SEQUENCE 137 AA; 15200 MW; ADD5881BP44B8EC9 CRC64;

Query Match 48.3%; Score 325.5; DB 1; Length 137;
Best Local Similarity 49.2%; Pred. No. 3.1e-27;
Matches 61; Conservative 23; Mismatches 31; Indels 9; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGRFNFVHVRQAPGQRFWMGWINPYNKPEFSK 60
DB 23 LQSGAEVKKPGASVKVSQASGRFNFVHVRQAPGQRFWMGWINPYNKPEFSK 82
QY 61 FQDRVTFTADTSANTAYNELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FRKATLAIKPSSTAYNQLSLTSSEDSAVYICARY-----RLGRVFDYWGQGTTL 133
QY 121 IVSS 124
DB 134 TVSS 137

RESULT 13
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P0380;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
CX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igd-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).

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Db 4 LVQSGAEVKPGSSVKVSKASGCTPERSAIHWVRQAPGGGLEWGMGIVPMFPNPAQK 63
Qy 61 FQDRVTFADTSANTAYMELSLRSADTAVYCA-RVGPYSWDDSPQDNYMDVWGKGT 119
Db 64 FQGRVTFADSTNTAYMELSLRSADTAVYCAAGGYGIV-----SPEEY-----NGGL 112
Qy 120 IVSS 124
Db 113 TVSS 117

RESULT 16
HV1F_HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region Mot.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86203277; PubMed=3084950;
RA Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RL immunoglobulin (Mot) having unusual papain cleavage sites.";
RL Mol. Immunol. 23:169-174(1986).
DR PIR; A02025; HVHUMO.
DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006985; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS0835; IG LIKE; 1.
DR IMGT; IMGT00110; Ig-like.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT NON_TER 99 107 D SEGMENT.
FT DOMAIN 108 125 J SEGMENT.
FT DISULFID 22 96
FT NON_TER 125 125 BY SIMILARITY.
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 47.3%; Score 319; DB 1; Length 125;
Best Local Similarity 50.8%; Pred. No. 1.4e-26;
Matches 63; Conservative 19; Mismatches 40; Indels 2; Gaps 1;

Qy 1 LEQSGAEVKPGASVKVSKASGYRFSNFIHWVRQAPGQRFEMWGNPYNGKETSFAK 60
Db 4 LVQSGAEVKPGSSARISCKVSGDFTYDIHWVRQAPGRLWMAVHPSDRTTYGPR 63
Qy 61 FQDRVTFADTSANTAYMELSLRSADTAVYCA-RVGPYSWDDSPQDNYMDVWGKGT 120
Db 64 SQARFTVTRDSSTTVYMTLTISADTAIYCAARGHYS--DTDDSGTSLGPWGQGTLL 121
Qy 121 IVSS 124
Db 122 IVSS 125

RESULT 17
HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RL region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVMS11.
DR HSSP; P01810; 2F8J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 121 121
SQ SEQUENCE 121-AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 47.2%; Score 318; DB 1; Length 121;
Best Local Similarity 50.0%; Pred. No. 1.7e-26;
Matches 62; Conservative 26; Mismatches 30; Indels 6; Gaps 3;

Qy 1 LEQSGAEVKPGASVKVSKASGYRFSNFIHWVRQAPGQRFEMWGNPYNGKETSFAK 60
Db 4 LQSGAEIVRPGTSVKISCKAAGTFTNYIGWKRPGHGLEWIGDIPGCGTNTINDN 63
Qy 61 FQDRVTFADTSANTAYMELSLRSADTAVYCA-RVGPYSWDDSPQDNYMDVWGKGT 120
Db 64 LKGKATLTADTSSSTAVIQLSLTSSEDSAIYHCA-RGIY-YNSSP----YFDSWGQGTLL 117
Qy 121 IVSS 124
Db 118 TVSS 121

RESULT 18
HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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RESULT 26
HV10 MOUSE
ID_HV10 MOUSE
STANDARD;
PRT; 117 AA.

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job time : 8.34815 secs

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:32:07 ; Search time 53.5333 Seconds
(without alignments)
770.584 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MEWSWFLPFLSVTTGVHSQ.....PDQNYMDVWGKGTIVVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing-first 100 summaries

Database : A Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	793	100.0	146	2	AAW01228 VH region
2	793	100.0	146	3	AAAY98285 Modified
3	793	100.0	146	3	AAAY95176 Modified
4	793	100.0	146	7	AADE06734 Human IGG
5	793	100.0	476	7	ABR61564 Human Mab
6	667	84.1	124	2	AAAR54244 Anti-HIV
7	667	84.1	124	2	AAAR75568 VH Fab MT
8	667	84.1	124	2	AAAW01227 VH region
9	667	84.1	124	3	AAAY98206 Anti-gp12
10	667	84.1	124	3	AAAY95097 Anti-gp12
11	659	83.1	250	3	AAAY44346 3B3 anti-b
12	657	82.8	124	2	AAAR75604 VH Fab H4
13	655	82.7	124	2	AAAR75605 VH Fab H4
14	653	82.3	124	2	AAAR54245 Anti-HIV
15	653	82.3	124	3	AAAW01246 VH region
16	653	82.3	124	3	AAAY98207 Anti-gp12
17	650	82.0	124	3	AAAY95098 Anti-gp12
18	650	82.0	124	2	AAAR75607 VH Fab H4
19	650	82.0	124	2	AAAR75608 VH Fab H4
20	649	81.8	124	2	AAAR54245 Anti-HIV
21	649	81.8	124	2	AAAW01247 VH region
22	649	81.8	124	3	AAAY98208 Anti-gp12
23	649	81.8	124	3	AAAY95099 Anti-gp12
24	648	81.7	124	2	AAAR75606 VH Fab H4
25	648	81.7	124	2	AAAR75609 VH Fab H4

26	646	81.5	124	2	AAAR75572 VH Fab 3b
27	645	81.3	124	2	AAAR75570 VH Fab 3b
28	641.5	80.9	124	2	AAAR54335 Anti-HIV
29	641.5	80.9	124	2	AAW01309 VH region
30	641.5	80.9	124	3	AAAY98270 Anti-gp12
31	641.5	80.9	124	3	AAAY95161 Anti-gp12
32	635	80.1	124	2	AAAR75569 VH Fab 3b
33	622.5	78.5	123	2	AAAR75571 VH Fab 3b
34	619	78.1	124	2	AAAR75617 VH Fab M5
35	619	78.1	124	2	AAAR75616 VH Fab M5
36	618	77.9	124	2	AAAR75615 VH Fab M5
37	612	77.2	124	2	AAAR75610 VH Fab M5
38	612	77.2	124	2	AAAR75613 VH Fab M5
39	611	77.0	124	2	AAAR75611 VH Fab M5
40	610	76.9	124	2	AAAR75612 VH Fab M5
41	610	76.9	124	2	AAAR75614 VH Fab M5
42	600	75.7	124	2	AAAR75640 VH Fab H1
43	599	75.5	124	2	AAAR75638 VH Fab H3
44	599	75.5	124	2	AAAR75641 VH Fab H1
45	598	75.4	124	2	AAAR75639 VH Fab H3
46	572.5	72.2	124	2	AAAR54331 Anti-HIV
47	572.5	72.2	124	2	AAW01305 VH region
48	572.5	72.2	124	3	AAAY98266 Anti-gp12
49	572.5	72.2	124	3	AAAY95157 Anti-gp12
50	549.5	69.3	124	2	AAAR54330 Anti-HIV
51	549.5	69.3	124	2	AAAR54336 Anti-HIV
52	549.5	69.3	124	2	AAW01310 VH region
53	549.5	69.3	124	2	AAW01304 VH region
54	549.5	69.3	124	3	AAAY98271 Anti-gp12
55	549.5	69.3	124	3	AAAY98265 Anti-gp12
56	549.5	69.3	124	3	AAAY95156 Anti-gp12
57	549.5	69.3	124	3	AAAY95162 Anti-gp12
58	543.5	68.5	125	2	AAAR54333 Anti-HIV
59	543.5	68.5	125	2	AAAR54268 Anti-HIV
60	543.5	68.5	125	2	AAW01307 VH region
61	543.5	68.5	125	2	AAW01303 VH region
62	543.5	68.5	125	3	AAAY98268 Anti-gp12
63	543.5	68.5	125	3	AAAY98264 Anti-gp12
64	543.5	68.5	125	3	AAAY95159 Anti-gp12
65	543.5	68.5	125	3	AAAY95155 Anti-gp12
66	540.5	68.2	124	2	AAAR54332 Anti-HIV
67	540.5	68.2	124	2	AAW01306 VH region
68	540.5	68.2	124	3	AAAY98267 Anti-gp12
69	540.5	68.2	124	3	AAAY95158 Anti-HIV
70	536.5	67.7	126	3	AAAY98263 Anti-gp12
71	536.5	67.7	126	3	AAAY95154 Anti-gp12
72	536.5	67.7	126	3	AAAY95154 Anti-gp12
73	533.5	67.3	124	2	AAAR54269 Anti-HIV
74	533.5	67.3	124	2	AAW01311 VH region
75	533.5	67.3	124	3	AAAY98272 Anti-gp12
76	533.5	67.3	124	3	AAAY95163 Anti-gp12
77	533.5	67.3	126	2	AAW01302 VH region
78	531.5	67.0	249	2	AAAR77610 Humanised
79	528.5	66.6	139	2	AAAR33953 GH1 varia
80	528.5	66.6	139	2	AAW29753 CDR-graft
81	528.5	66.6	139	3	AAAY56877 GH1 varia
82	528.5	66.6	125	2	AAAR54334 Anti-HIV
83	522.5	65.9	125	2	AAW01308 VH region
84	522.5	65.9	125	3	AAAY98269 Anti-gp12
85	522.5	65.9	125	3	AAAY95160 Anti-gp12
86	522.5	65.9	125	2	AAAR77615 Humanised
87	522	65.8	140	2	AAW21847 Humanised
88	520.5	65.6	249	2	AAAR77611 Humanised
89	510	64.3	140	2	AAW21849 Humanised
90	506	63.8	140	2	AAAR64235 Humanized
91	506	63.8	140	2	AAAR64265 CDR-graft
92	506	63.8	470	5	AAU74296 Anti-huma
93	504	63.6	146	2	AAW22841 Human ant
94	501.5	63.2	137	3	AAAY98847 Humanised
95	500.5	63.1	588	3	AAW71880 Anti-huma
96	500.5	63.1	588	3	AAW12917 Anti-huma
97	498.5	62.9	135	2	AAAR24107 Humanised
98	498	62.8	140	2	AAW21850 Humanised

CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 XX Sequence 146 AA;

Query Match 100.0%; Score 793; DB 3; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.4e-68;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFVHVRQAP 60
 DB 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFVHVRQAP 60
 QY 61 GQFEWGWINPYNGNKEFSKQFDRVTFADTSANTAYMELSLRSADTAVYCARVGP 120
 DB 61 GQFEWGWINPYNGNKEFSKQFDRVTFADTSANTAYMELSLRSADTAVYCARVGP 120
 QY 121 YSWDDSPQDNYMDVWGKGTIVSS 146
 DB 121 YSWDDSPQDNYMDVWGKGTIVSS 146

RESULT 3
 AAY95176
 ID AAY95176 standard; protein; 146 AA.
 XX
 XX AAY95176;
 XX
 DT 30-JUN-2000 (first entry)
 XX
 DE Modified heavy chain variable region amino acid sequence.
 XX
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; Glycoprotein 41; gp41; monoclonal antibody.
 XX
 XX Synthetic.
 XX
 XX AU948756-A.
 XX
 XX 17-FEB-2000.
 XX
 XX 16-SEP-1999; 99AU-00048756.
 XX
 XX 16-SEP-1999; 99AU-00048756.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 2000-293393/26.
 XX
 XX Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX
 XX Example 4; Page 111; 366pp; English.

XX
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and

CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 XX Sequence 146 AA;

Query Match 100.0%; Score 793; DB 3; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.4e-68;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFVHVRQAP 60
 DB 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFVHVRQAP 60
 QY 61 GQFEWGWINPYNGNKEFSKQFDRVTFADTSANTAYMELSLRSADTAVYCARVGP 120
 DB 61 GQFEWGWINPYNGNKEFSKQFDRVTFADTSANTAYMELSLRSADTAVYCARVGP 120
 QY 121 YSWDDSPQDNYMDVWGKGTIVSS 146
 DB 121 YSWDDSPQDNYMDVWGKGTIVSS 146

RESULT 4
 ADE06734
 ID ADE06734 standard; protein; 146 AA.
 XX
 XX ADE06734;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human IgG Fab b12 heavy chain protein SEQ ID NO:4.
 XX
 XX hybrid polypeptide; protein aggregation; prion polypeptide;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant;
 KW cerebroprotective; antiparkinsonian; cycostatic; nephrotropic; cardiant;
 KW antiinflammatory; antiarteriosclerotic; gene therapy;
 KW Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
 KW Alzheimer's disease; Type II diabetes; Huntington's disease;
 KW immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
 KW amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
 KW Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
 KW familial amyloidotic polyneuropathy; medullary carcinoma;
 KW chronic renal failure; congestive heart failure; chronic inflammation;
 KW atherosclerosis; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003085086-A2.
 XX
 XX 16-OCT-2003.
 XX
 XX 08-APR-2003; 2003WO-US010856.
 PF
 XX 09-APR-2002; 2002US-0371610P.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA

XX Burton DR, Williamson RA, Moroncini G;
XX WPI: 2003-877028/81.
XX N-PSDB; ADE06733.
XX
XX New motif-grafted hybrid polypeptides binding to the infectious form of a
XX prion, useful for diagnosing or treating diseases of protein aggregation
XX or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
XX diabetes.
XX
XX Claim 37; SEQ ID NO 4; 115pp; English.
XX
XX The present invention describes a hybrid polypeptide (I) comprising: (a)
XX a polypeptide motif containing a sufficient number of contiguous amino
XX acid residues from a polypeptide associated with a disease of protein
XX aggregation or conformation to bind an aggregating form of the
XX polypeptide or to a disease-associate conformer of the polypeptide; and
XX (b) an additional amino acids from a polypeptide other than the
XX polypeptide from which the motif is derived, where the resulting hybrid
XX polypeptide binds with greater affinity to a disease causing or
XX infectious conformer of the polypeptide than is the source of the
XX polypeptide motif compared to a benign form of the polypeptide. Also
XX described: (1) a nucleic acid molecule encoding (I); (2) a vector
XX comprising the nucleic acid molecule; (3) a cell comprising the vector;
XX (4) detecting an isoform or a PfSC form of a prion polypeptide or a
XX polypeptide associated with a disease of protein aggregation, in a sample
XX; (5) a solid support comprising a plurality of polypeptides described
XX above; (6) detecting cells that contain a protein conformer associated
XX with a disease of protein aggregation; (7) preparing a hybrid molecule
XX that specifically interacts with one conformer of a protein involved in
XX the disease mentioned above; and (8) an anti-idiotypic antibody that
XX specifically binds to an infectious form of a prion protein. (I) has
XX neuroprotective, neurotropic, antidiabetic, anticonvulsant,
XX cerebroprotective, antiparkinsonian, cytoskeletal, neurotropic, cardiac,
XX anti-inflammatory and antiarteriosclerotic activities, and can be used in
XX gene therapy. The composition and methods of the present invention can be
XX used in diagnosing or treating diseases of protein aggregation or
XX conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine
XX spongiform encephalopathy, Alzheimer's disease, Type II diabetes,
XX Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis
XX associated with chronic inflammatory disease, hereditary systemic
XX amyloidosis associated with autosomal dominant inheritance of variant
XX transthyretin gene, amyotrophic lateral sclerosis, Pick's disease,
XX Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma
XX cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma
XX of thyroid, chronic renal failure, congestive heart failure, senile
XX cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis
XX or familial amyloidosis. The present sequence is used in the
XX exemplification of the present invention.
XX
XX Sequence 146 AA;
XX
XX Query Match 100.0%; Score 793; DB 7; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-68;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MENSWFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAP 60
XX
XX 1 MENSWFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAP 60
XX
XX 61 GQRFEMGWINPYNNGKFSKQDRVTFTADTSANTATMELSLRSADTAVYYCARVGP 120
XX
XX 61 GQRFEMGWINPYNNGKFSKQDRVTFTADTSANTATMELSLRSADTAVYYCARVGP 120
XX
XX 121 YSWDDSPQDNYMDVNGKGTIVSS 146
XX
XX 121 YSWDDSPQDNYMDVNGKGTIVSS 146
XX
XX
XX RESULT 5
XX ABR61564
XX ID ABR61564 standard; protein; 476 AA.

XX ABR61564;
XX AC
XX 15-JAN-2004 (first entry)
XX
XX Human MAb IgG1b12 heavy chain.
XX
XX Adeno-associated virus; rAAV; IgG1b12; ScFvX5; anti-HIV; antibacterial;
XX antirheumatic; antiarthritic; cytostatic; sedative; antiinflammatory;
XX neuroprotective; gene therapy; vaccine; antibody; Mab.
XX
XX Homo sapiens.
XX
XX WC2003087324-A2.
XX 23-OCT-2003.
XX
XX 09-APR-2003; 2003WO-US010865.
XX
XX 09-APR-2002; 2002US-0371501P.
XX (CHIL-) CHILDRENS HOSPITAL INC.
XX
XX Clark KR; Johnson PR;
XX
XX WPI: 2003-833721/77.
XX N-PSDB; ACF58045.
XX
XX New recombinant adeno-associated virus (rAAV)/IgG1b12 or rAAV/ScFvX5
XX genome, useful for preventing or treating viral infections (e.g. HIV),
XX bacterial infections or other chronic disease states (e.g. cancer,
XX inflammation or kuru).
XX
XX Example 1; Page 35-37; Opp; English.
XX
XX The invention relates to a recombinant adeno-associated virus (rAAV)/
XX IgG1b12 or rAAV/ScFvX5 genome. The rAAV is useful for gene delivery,
XX particularly in delivering antibody genes to target cells in mammals. The
XX antibodies may be used to prevent and/or treat viral infections
XX (particularly HIV), bacterial infections and other chronic disease states
XX (e.g. cancer, rheumatoid arthritis, inflammation, fatal familial
XX insomia, kuru, Mad Cow Disease or Alpers syndrome). The present sequence
XX represents the human monoclonal antibody (Mab) IgG1b12 heavy chain
XX
XX Sequence 476 AA;
XX
XX Query Match 100.0%; Score 793; DB 7; Length 476;
XX Best Local Similarity 100.0%; Pred. No. 5.4e-68;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MENSWFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAP 60
XX
XX 1 MENSWFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAP 60
XX
XX 61 GQRFEMGWINPYNNGKFSKQDRVTFTADTSANTATMELSLRSADTAVYYCARVGP 120
XX
XX 61 GQRFEMGWINPYNNGKFSKQDRVTFTADTSANTATMELSLRSADTAVYYCARVGP 120
XX
XX 121 YSWDDSPQDNYMDVNGKGTIVSS 146
XX
XX 121 YSWDDSPQDNYMDVNGKGTIVSS 146
XX
XX
XX RESULT 6
XX AAR54244
XX ID AAR54244 standard; protein; 124 AA.
XX
XX AAR54244;
XX
XX 25-MAR-2003 (revised)
XX 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin heavy chain variable region b4.

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XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; heavy chain; variable region;
KW framework region; complementarity determining region.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..27
FT Region /label= FR1
FT Region 28..32
FT Region /label= CDR1
FT Region 33..46
FT Region /label= FR2
FT Region 47..63
FT Region /label= CDR2
FT Region 64..95
FT Region /label= FR3
FT Region 96..113
FT Region /label= CDR3
FT Region 114..124
FT Region /label= FR4
XX WO9407922-A1.
XX 14-APR-1994.
XX 30-SEP-1993; 93WO-US009328.
XX 30-SEP-1992; 92US-00954148.
XX (SCRI ) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 1994-135516/16.
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX Claim 1; Page 163-164; 248pp; English.
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli Xli Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAB regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The heavy chain VH region sequence AAR54244
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 124 AA;
SQ
Query Match 84.1%; Score 667; DB 2; Length 124;
Best Local Similarity 99.2%; Pred. No. 1.6e-56;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFPMWGNIPYNGKFSK 82
Dd 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFPMWGNIPYNGKFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Dd 61 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Dd 121 IVSS 124
RESULT 7
AAR/5568

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ID AAR75568 standard; protein; 124 AA.
XX AAR/5568;
XX 05-MAR-1996 (first entry)
XX VH Fab MT4 binds to gp120.
XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAb;
KW immunoreaction; neutralisation; passive immunotherapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..27
FT Region /label= FR1
FT Region 28..32
FT Region /label= CDR1
FT Region 33..46
FT Region /label= FR2
FT Region 47..63
FT Region /label= CDR2
FT Region 64..95
FT Region /label= FR3
FT Region 96..113
FT Region /label= CDR3
FT Region 114..124
FT Region /label= FR4
XX WO9511317-A1.
XX 27-APR-1995.
XX 19-OCT-1994; 94WO-US011907.
XX 19-OCT-1993; 93US-00139409.
PR 26-APR-1994; 94US-00233619.
PR 19-SEP-1994; 94US-00308841.
XX (SCRI ) SCRIPPS RES INST.
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1995-170235/22.
DR N-PSDB; AAQ92540.
XX Synthetic human neutralising monoclonal antibodies to human
PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
PT induced disease.
XX Claim 9; Page 170; 249pp; English.
XX The sequences given in AAR75568-72 represent human Fab's comprising
CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
CC have randomised amino acids in the entire CDR1 and in four of the 18
CC amino acid residues in CDR3. These Fab's are used in the production of a
CC human monoclonal antibody (MAB) which is capable of immunoreacting with,
CC and neutralising HIV. The MAB's are capable of reducing HIV infectivity
CC titre in an in vitro virus infectivity assay by 50% at a concentration of
CC <100 ng of antibody per ml. They can be used to provide passive
CC immunotherapy to HIV in a human. They neutralise HIV more effectively
CC than antibodies selected from non-randomised combinatorial libraries
XX Sequence 124 AA;
SQ
Query Match 84.1%; Score 667; DB 2; Length 124;
Best Local Similarity 99.2%; Pred. No. 1.6e-56;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFPMWGNIPYNGKFSK 82

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Db 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKSFSAK 60
 QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 Db 121 IVSS 124
 RESULT 8
 AAW01227
 ID AAW01227 standard; protein, 124 AA.
 AC AAW01227;
 XX
 XX 27-JAN-1997 (first entry)
 XX
 XX VH region of HIV neutralising MAb, clones b4 and b12.
 XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4
 XX
 XX WO9602273-A1.
 XX
 XX 01-FEB-1996.
 XX
 XX 11-JUL-1995; 95WO-US008743.
 XX
 XX 18-JUL-1994; 94US-00276852.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 1996-179601/18.
 XX
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 XX immunotherapy and detection of HIV infection.
 XX
 XX Claim 9; Fig 10; 366pp; English.
 XX
 XX This sequence represents the heavy chain variable region (VH) of a
 XX monoclonal antibody (MAb) which is immunoreactive with HIV glycoprotein
 XX gp120 and is capable of neutralising HIV. This sequence represents the
 XX sequence of clones b4 and b12. The MAb has the capacity to reduce HIV
 XX infectivity titre in an in vivo virus infectivity assay by 50 % at a
 XX concentration of less than 700 ng of antibody/ml, and binds mature gp120
 XX preferentially over the precursor gp160. This sequence forms the heavy
 XX chain component of MAb's with the light chain sequences given in
 XX AAW01273, AAW01275-76, AAW01296, and AAW01299-300. The MAb may
 XX be used for determining immunocompetence of a human anti-HIV antibody and

CC in the detection of HIV infection
 XX
 SQ Sequence 124 AA;
 Query Match 84.1%; Score 667; DB 2; Length 124;
 Best Local Similarity 99.2%; Pred. No. 1.6e-56;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKSFSAK 82
 Db 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKSFSAK 60
 QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 Db 121 IVSS 124
 RESULT 9
 AAY98206
 ID AAY98206 standard; protein, 124 AA.
 XX
 AC AAY98206;
 XX
 XX 04-JUL-2000 (first entry)
 XX
 XX Anti-gp120 antibody heavy chain variable region from clone b4.
 XX
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 XX AU9948754-A.
 XX
 XX 17-FEB-2000.
 XX
 XX 16-SEP-1999; 99AU-00048754.
 XX
 XX 16-SEP-1999; 99AU-00048754.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 2000-246867/22.
 XX
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 XX (HIV) used for providing passive immunotherapy to HIV are specific for
 XX glycoprotein-120.
 XX
 XX Claim 1; Fig 10; 374pp; English.
 XX
 XX This sequence represents a fragment of the antibodies of the invention.
 XX The invention relates to the production of an anti-HIV (human
 XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 XX of reducing an HIV infectivity titre in an in vitro virus infectivity
 XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
 XX production of the antibody comprises: (a) providing a first
 XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 XX (which does not comprise the sequence represented by AAY98206) and a
 XX second polynucleotide encoding a light chain immunoglobulin amino acid
 XX sequence; (b) inserting the first and second polynucleotide sequences
 XX into a host cell; (c) maintaining the host cell in conditions which allow
 XX the amino acid sequences encoded by the polynucleotides to be expressed
 XX in the host cell; and (d) isolating the antibody comprising the heavy and
 XX light chain immunoglobulin amino acid sequences from the host cell. The
 XX anti-HIV gp-120 monoclonal antibody is used for providing passive

CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation. Note: The present sequence is specifically not claimed
 XX
 SQ Sequence 124 AA;

Query Match 84.1%; Score 667; DB 3; Length 124;
 Best Local Similarity 99.2%; Pred. No. 1.6e-56;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFVWGMWNPYNGNKEFSK 82
 DB 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFVWGMWNPYNGNKEFSK 60

QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 11
 AAY95097
 ID AAY95097 standard; protein; 124 AA.
 AC AAY95097;
 XX 30-JUN-2000 (first entry)
 DT Anti-gp120 antibody heavy chain variable region from clone b4.
 DE Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX Homo sapiens.
 XX AU9948756-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048756.
 XX 16-SEP-1999; 99AU-00048756.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-293393/26.
 XX Novel human monoclonal antibodies which immunoreact with and neutralize
 XX human immunodeficiency virus useful for treating HIV infections.
 XX Example 9; Fig 10; 366pp; English.
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to

CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 SQ Sequence 124 AA;

Query Match 84.1%; Score 667; DB 3; Length 124;
 Best Local Similarity 99.2%; Pred. No. 1.6e-56;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFVWGMWNPYNGNKEFSK 82
 DB 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFVWGMWNPYNGNKEFSK 60

QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 11
 AAY44346
 ID AAY44346 standard; protein; 250 AA.
 AC AAY44346;
 XX 14-MAR-2000 (first entry)
 DT 3B3 antibody.
 DE 3B3 antibody; immunotoxin; variable fragment; Fv; gp120 coat protein;
 KW exotoxin; PE38; Human immunodeficiency virus type 1; HIV-1; specificity;
 KW combinatorial phage display library; bone marrow RNA; connector peptide;
 KW cytotoxic moiety; transformed cell line; transplant; quantify.
 XX Homo sapiens.
 XX Key
 XX Key
 XX Peptide
 XX 129..143
 XX /label= Linker peptide
 XX /note= "Links VH and VL regions of 3B3 antibody"
 XX WO9964073-A2.
 XX 16-DEC-1999.
 XX 08-JUN-1999; 99WO-US012909.
 XX 11-JUN-1998; 98US-0088860P.

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XX (USSH ) US DRPT HEALTH & HUMAN SERVICES.
PA Pastan IH, Bera TK, Kennedy PE, Berger EA, Barbas CF;
XX WPI; 2000-105833/09.
DR N-PSDB; AAZ29448.
XX Novel recombinant immunotoxin directed against the HIV- 1 gp120 coat
FT protein useful for treating HIV-1 infections.
XX Claim 17; Page 47; 50pp; English.
XX The present amino acid sequence is the variable fragment (Fv) of 3B3
CC antibody, isolated from a combinatorial phage display library constructed
CC from bone marrow RNA of an infected individual. It is used in a novel
CC chimeric immunotoxin, that comprises an anti-gp120 antibody, having
CC binding specificity to 3B3(Fv) antibody, that is attached by a connector
CC peptide to a cytotoxic moiety, PE38 derived from P.aeruginosa. The
CC chimeric immunotoxin is used in the treatment of HIV-1 infections. It is
CC capable of specifically targeting and killing cells displaying HIV-1
CC gp120 coat protein. They can be used ex vivo to reduce and/or eliminate
CC the HIV viral load in the infected cells. It can also be used in
CC establishing transformed cell lines derived from HIV-infected sources.
CC The immunotoxins can also be used for detecting the presence or absence
CC and for quantifying the infected cells
XX Sequence 250 AA;
SQ
Query Match      83.1%; Score 659; DB 3; Length 250;
Best Local Similarity 95.3%; Pred. No. 2.2e-55;
Matches 121; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 20 QVQLVQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVRQAPGQRFVWGMGINPYNKKEF 79
DB 2 QVLEQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVRQAPGQRFVWGMGINPYNKKEF 61
QY 80 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKG 139
DB 62 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKG 121
QY 140 TTVIVSS 146
DB 122 TTVIVSS 128
RESULT 12
AAR75604
ID AAR75604 standard; protein; 124 AA.
XX
AC AAR75604;
XX
XX 11-MAR-1996 (first entry)
DT
XX VH Fab H4H1-1 binds to gp120.
DE
XX Human, Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; 3b9; M74; humanised; monoclonal antibody; Mab;
KW immunoreaction; neutralisation; passive immunotherapy.
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
PH 1. .27
FT Region /label= FR1
FT Region 28. .32
FT Region /label= CDR1
FT Region 33. .46
FT Region /label= FR2
FT Region 47. .63
FT Region /label= CDR2
FT Region 64. .95
FT /label= FR3

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FT Region 96. .113
FT /label= CDR3
FT Region 114. .124
FT /label= FR4
XX
XX WO9511317-A1.
XX
XX 27-APR-1995.
XX
XX 19-OCT-1994; 94WO-US011907.
XX
XX 19-OCT-1993; 93US-00139409.
XX 26-APR-1994; 94US-00233619.
XX 19-SEP-1994; 94US-00308841.
XX (SCRI ) SCRIPPS RES INST.
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1995-170235/22.
XX Synthetic human neutralising monoclonal antibodies to human
FT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
FT induced disease.
XX
XX Example 4B1; Fig 7; 249pp; English.
XX
XX The sequences given in AAR75604-09 represent human Fab's comprising
CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
CC sequences containing the preferred His residue as the first residue of
CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
CC used in the production of a human monoclonal antibody (Mab) which is
CC capable of immunoreacting with, and neutralising HIV. The Mab's are
CC capable of reducing HIV infectivity titre in an in vitro virus
CC infectivity assay by 5% at a concentration of <100 ng of antibody per
CC ml. They can be used to provide passive immunotherapy to HIV in a human.
CC They neutralise HIV more effectively than antibodies selected from non-
CC randomised combinatorial libraries
XX Sequence 124 AA;
SQ
Query Match      82.8%; Score 657; DB 2; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.5e-55;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVRQAPGQRFVWGMGINPYNKKEFSAK 82
DB 1 LEQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVRQAPGQRFVWGMGINPYNKKEFSAK 60
QY 83 FQDRVTFTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
DB 121 IVSS 124
RESULT 13
AAR75605
ID AAR75605 standard; protein; 124 AA.
XX
AC AAR75605;
XX
XX 11-MAR-1996 (first entry)
DT
XX VH Fab H4H1-3 binds to gp120.
DE
XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; 3b9; M74; humanised; monoclonal antibody; Mab;
KW immunoreaction; neutralisation; passive immunotherapy.
XX

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OS Synthetic.
XX Key Location/Qualifiers
XX FH 1. .27
XX FT Region /label= FR1
XX FT Region 28. .32
XX FT Region /label= CDR1
XX FT Region 33. .46
XX FT Region /label= FR2
XX FT Region 47. .63
XX FT Region /label= CDR2
XX FT Region 64. .95
XX FT Region /label= FR3
XX FT Region 96. .113
XX FT Region /label= CDR3
XX FT Region 114. .124
XX FT Region /label= FR4
XX PN WO9511317-A1.
XX DD 27-APR-1995.
XX PF 19-OCT-1994; 94WO-US011907.
XX PR 19-OCT-1993; 93US-00139409.
XX PR 26-APR-1994; 94US-00233619.
XX PR 19-SEP-1994; 94US-00308841.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX PI WPI; 1995-170235/22.
XX DR Synthetic human neutralising monoclonal antibodies to human
XX FT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX FT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX CC The sequences given in AAR75604-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (WAB) which is
XX CC capable of immunoreacting with, and neutralising HIV. The Mab's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SQ Sequence 124 AA;
XX Query Match 82.7%; Score 656; DB 2; Length 124;
XX Best Local Similarity 96.8%; Pred. No. 1.9e-55;
XX Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX QY 23 LVQSGAEVKKPGASVKVSCQASGVRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSK 82
XX DB 1 LEQSGAEVKKPGASVKVSCQASGVRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
XX QY 83 FQDRVTFADTSAANTAYMELRLSRSDATVAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
XX DB 61 FQDRVTFADTSAANTAYMELRLSRSDATVAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
XX QY 143 IVSS 146
XX DB 121 IVSS 124
XX RESULT 14

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AAR54245
ID AAR54245 standard; protein; 124 AA.
XX AC AAR54245;
XX DT 25-MAR-2003 (revised)
XX DT 10-NOV-1994 (first entry)
XX DE Anti-HIV gp120 immunoglobulin heavy chain variable region b7.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX KW neutralisation; monoclonal antibody; heavy chain; variable region;
XX KW framework region; complementarity determining region.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 1. .27
XX FT Region /label= FR1
XX FT Region 28. .32
XX FT Region /label= CDR1
XX FT Region 33. .46
XX FT Region /label= FR2
XX FT Region 47. .63
XX FT Region /label= CDR2
XX FT Region 64. .95
XX FT Region /label= FR3
XX FT Region 96. .113
XX FT Region /label= CDR3
XX FT Region 114. .124
XX FT Region /label= FR4
XX PN WO9407922-A1.
XX DD 14-APR-1994.
XX PF 30-SEP-1993; 93WO-US009328.
XX PR 30-SEP-1992; 92US-00954148.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1994-135516/16.
XX PT New human monoclonal antibodies neutralising HIV - react with gp120 or
XX PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX PT diagnosis and for passive immuno-therapy.
XX PS Claim 1; Page 164; 248pp; English.
XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX CC using primers specific for heavy and light chain variable regions. The
XX CC amplification products were inserted into a dicistronic vector to produce
XX CC a library of fragments. E.coli XLI Blue cells were transformed with the
XX CC library. Filamentous phage were produced which expressed the Mab regions
XX CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX CC immunoreactive clones. The heavy chain VH region sequence AAR54245
XX CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 124 AA;
XX Query Match 82.3%; Score 653; DB 2; Length 124;
XX Best Local Similarity 96.0%; Pred. No. 3.7e-55;
XX Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX QY 23 LVQSGAEVKKPGASVKVSCQASGVRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSK 82
XX DB 1 LEQSGAEVKKPGASVKVSCQASGVRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
XX QY 83 FQDRVTFADTSAANTAYMELRLSRSDATVAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142

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Db 61 FQDRVTFTADTANTAYMELSLRSADTAIYCARVGPYTWDDSPQDNYMDVWGKTKV 120
 QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 15
 AAW01246
 ID AAW01246 standard; protein; 124 AA.
 XX
 AC AAW01246;
 XX
 DT 28-JAN-1997 (first entry)
 XX
 DE VH region of HIV neutralising MAb, IgG1 b7.
 XX
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4
 XX WO9602273-A1.
 XX
 PD 01-FEB-1996.
 XX
 PD 11-JUL-1995; 95WO-US008743.
 XX
 PD 18-JUL-1994; 94US-00276852.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 WI WPI; 1996-179601/18.
 XX
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.
 XX
 PS Example; Fig 10; 366pp; English.
 XX
 CC The sequences given in AAW01233-60 represent the heavy chain variable
 CC regions (VH) of a series of monoclonal antibodies (MAb's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JH6 gene
 CC clone, b7. A MAb containing this VH sequence has the capacity to reduce
 CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. The MAb may be used for
 CC determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection
 CC
 XX Sequence 124 AA;
 SQ Query Match 82.3%; Score 653; DB 2; Length 124;

Best Local Similarity 96.0%; Pred. No. 3.7e-55;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFVWGWINPYNKFSK 82
 Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFVWGWINPYNKFSK 60

QY 83 FQDRVTFTADTANTAYMELSLRSADTAIYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 Db 61 FQDRVTFTADTANTAYMELSLRSADTAIYCARVGPYTWDDSPQDNYMDVWGKTKV 120

QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 16
 AAY98207
 ID AAY98207 standard; protein; 124 AA.
 XX
 AC AAY98207;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Anti-gp120 antibody heavy chain variable region from clone b7.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU9948754-A.
 XX
 PD 17-FEB-2000.
 XX
 PD 16-SEP-1999; 99AU-00048754.
 XX
 PD 16-SEP-1999; 99AU-00048754.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 WI WPI; 2000-246867/22.
 XX
 PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 PS Example 9; Fig 10; 374pp; English.
 XX
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV

CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 CC
 SQ Sequence 124 AA;

Query Match 82.3%; Score 653; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 3.7e-55;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 82
 Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 60

QY 83 FQDRVTFDTADTSANTAYMELRSLSADTAIYICARVGPYSWDDSPQDNYYMDVWGKGT 142
 Db 61 FQDRVTFDTADTSANTAYMELRSLSADTAIYICARVGPYSWDDSPQDNYYMDVWGKGT 120

QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 17

AA95098
 ID AA95098 standard; protein; 124 AA.

AC AA95098;

DT 30-JUN-2000 (first entry)

DE Anti-gp120 antibody heavy chain variable region from clone b7.

KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW Glycoprotein 120; gp120; Glycoprotein 41; gp41; monoclonal antibody.

OS Homo sapiens.

PN AU9948756-A.

PD 17-FEB-2000.

PF 16-SEP-1999; 99AU-00048756.

PR 16-SEP-1999; 99AU-00048756.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 2000-293393/26.

PT Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.

XX Example 9; Fig 10; 366pp; English.

PS The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature Glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and

CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp1 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 CC
 SQ Sequence 124 AA;

Query Match 82.3%; Score 653; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 3.7e-55;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 82
 Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 60

QY 83 FQDRVTFDTADTSANTAYMELRSLSADTAIYICARVGPYSWDDSPQDNYYMDVWGKGT 142
 Db 61 FQDRVTFDTADTSANTAYMELRSLSADTAIYICARVGPYSWDDSPQDNYYMDVWGKGT 120

QY 143 IVSS 146

Db 121 IVSS 124

RESULT 18

AA975607
 ID AA975607 standard; protein; 124 AA.

AC AA975607;

DT 11-MAR-1996 (first entry)

XX VH Fab H4H1-6 binds to gp120.

KW Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
 KW immunoreaction; neutralisation; passive immunotherapy.

OS Synthetic.

XX Key Location/Qualifiers

FT Region 1..27

FT /label= FR1

FT Region 28..32

FT /label= CDR1

FT Region 33..46

FT /label= FR2

FT Region 47..63

FT /label= CDR2

FT Region 64..95

FT /label= FR3

FT Region 96..113

FT /label= CDR3

FT Region 114..124

FT /label= FR4

PN WO9511317-A1.

XX


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XX DE Anti-HIV gp120 immunoglobulin heavy chain variable region b21.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX KW neutralisation; monoclonal antibody; heavy chain; variable region;
XX KW framework region; complementarity determining region.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..27
XX FT /label= FR1
XX FT Region
XX FT 28..32
XX FT /label= CDR1
XX FT Region
XX FT 33..46
XX FT /label= FR2
XX FT Region
XX FT 47..63
XX FT /label= CDR2
XX FT Region
XX FT 64..95
XX FT /label= FR3
XX FT Region
XX FT 96..113
XX FT /label= CDR3
XX FT Region
XX FT 114..124
XX FT /label= FR4
XX PN WO9407922-A1.
XX PD 14-APR-1994.
XX PF 30-SEP-1993; 93WO-US009328.
XX PR 30-SEP-1992; 92US-00954148.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1994-135516/16.
XX FT New human monoclonal antibodies neutralising HIV - react with gp120 or
XX FT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX FT diagnosis and for passive immuno-therapy.
XX PS Claim 1; Page 165; 248pp; English.
XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX CC using primers specific for heavy and light chain variable regions. The
XX CC amplification products were inserted into a dicistronic vector to produce
XX CC a library of fragments. E.coli Xli Blue cells were transformed with the
XX CC library. Filamentous phage were produced which expressed the MAb regions
XX CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX CC immunoreactive clones. The heavy chain VH region sequence AAR54246
XX CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 124 AA;
XX FT
XX FT Query Match 81.8%; Score 649; DB 2; Length 124;
XX FT Best Local Similarity 95.2%; Pred. No. 8.9e-55;
XX FT Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHHVRQAPGQRFQFWMGWINPYNKKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHHVRQAPGQRFQFWMGWINPYNKKEFSK 60
QY 83 FQDRVTEADTANTAYMEILSRSDATYVYCARVGYSDSDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTEADTANTAYMEILSRSDTATYVYCARVGYPTWDDSPQDNYMDVWGKTKV 120
QY 143 IVSS 146
DB 121 IVSS 124

```

```

XX DE Anti-HIV gp120 immunoglobulin heavy chain variable region b21.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX KW neutralisation; monoclonal antibody; heavy chain; variable region;
XX KW framework region; complementarity determining region.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..27
XX FT /label= FR1
XX FT Region
XX FT 28..32
XX FT /label= CDR1
XX FT Region
XX FT 33..46
XX FT /label= FR2
XX FT Region
XX FT 47..63
XX FT /label= CDR2
XX FT Region
XX FT 64..95
XX FT /label= FR3
XX FT Region
XX FT 96..113
XX FT /label= CDR3
XX FT Region
XX FT 114..124
XX FT /label= FR4
XX PN WO9407922-A1.
XX PD 14-APR-1994.
XX PF 30-SEP-1993; 93WO-US009328.
XX PR 30-SEP-1992; 92US-00954148.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1994-135516/16.
XX FT New human monoclonal antibodies neutralising HIV - react with gp120 or
XX FT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX FT diagnosis and for passive immuno-therapy.
XX PS Claim 1; Page 165; 248pp; English.
XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX CC using primers specific for heavy and light chain variable regions. The
XX CC amplification products were inserted into a dicistronic vector to produce
XX CC a library of fragments. E.coli Xli Blue cells were transformed with the
XX CC library. Filamentous phage were produced which expressed the MAB regions
XX CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX CC immunoreactive clones. The heavy chain VH region sequence AAR54246
XX CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 124 AA;
XX FT
XX FT Query Match 81.8%; Score 649; DB 2; Length 124;
XX FT Best Local Similarity 95.2%; Pred. No. 8.9e-55;
XX FT Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHHVRQAPGQRFQFWMGWINPYNKKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHHVRQAPGQRFQFWMGWINPYNKKEFSK 60
QY 83 FQDRVTEADTANTAYMEILSRSDATYVYCARVGYSDSDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTEADTANTAYMEILSRSDTATYVYCARVGYPTWDDSPQDNYMDVWGKTKV 120
QY 143 IVSS 146
DB 121 IVSS 124

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RESULT 21
AAW01247
ID AAW01247 standard; protein; 124 AA.
XX AC AAW01247;
XX DT 28-JAN-1997 (first entry)
XX DE VH region of HIV neutralising MAb, IgG1 b21.
XX KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
XX KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX KW virus infectivity assay; precursor; gp160; immunocompetence; human;
XX KW anti-HIV antibody; detection; HIV infection.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..27
XX FT /label= FR1
XX FT Region
XX FT 28..32
XX FT /label= CDR1
XX FT Region
XX FT 33..46
XX FT /label= FR2
XX FT Region
XX FT 47..63
XX FT /label= CDR2
XX FT Region
XX FT 64..95
XX FT /label= FR3
XX FT Region
XX FT 96..113
XX FT /label= CDR3
XX FT Region
XX FT 114..124
XX FT /label= FR4
XX PN WO9602273-A1.
XX PD 01-FEB-1996.
XX PR 11-JUL-1995; 95WO-US008743.
XX PR 18-JUL-1994; 94US-00276852.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1996-179601/18.
XX FT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
XX FT immuno:therapy and detection of HIV infection.
XX PS Example; Fig 10; 368pp; English.
XX CC The sequences given in AAW01233-60 represent the heavy chain variable
XX CC regions (VH) of a series of monoclonal antibodies (MAb's) which are
XX CC immunoreactive with HIV glycoprotein gp120 and are capable of
XX CC neutralising HIV. This sequence represents the sequence of the JH6 gene
XX CC clone, b21. A MAb containing this VH sequence has the capacity to reduce
XX CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
XX CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
XX CC preferentially over the precursor gp160. The MAb may be used for
XX CC determining immunocompetence of a human anti-HIV antibody and in the
XX CC detection of HIV infection
XX SQ Sequence 124 AA;
XX FT
XX FT Query Match 81.8%; Score 649; DB 2; Length 124;
XX FT Best Local Similarity 95.2%; Pred. No. 8.9e-55;
XX FT Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHHVRQAPGQRFQFWMGWINPYNKKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHHVRQAPGQRFQFWMGWINPYNKKEFSK 60

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QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 22
 AAY98208
 ID AAY98208 standard; protein; 124 AA.
 XX AC AAY98208;
 XX 04-JUL-2000 (first entry)
 DT Anti-gp120 antibody heavy chain variable region from clone b21.
 DE Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX Homo sapiens.
 CS
 OS
 FN AU9948754-A.
 XX 17-FEB-2000.
 PD
 FF 16-SEP-1999; 99AU-00048754.
 XX
 PR 16-SEP-1999; 99AU-00048754.
 XX (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-246867/22.
 DR Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 PS Example 9; Fig 10; 374pp; English.

This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and

CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 SQ Sequence 124 AA;
 Query Match 81.8%; Score 649; DB 3; Length 124;
 Best Local Similarity 95.2%; Freq. No. 8.9e-55;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSQASGVYRFSNFIHWVRQAPGQRFEMWGWINPYNKFSK 82
 Db 1 LEQSGAEVKKPGASVKVSQASGVYRFSNFIHWVRQAPGQRFEMWGWINPYNKFSK 60
 QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 23
 AAY95099
 ID AAY95099 standard; protein; 124 AA.
 XX AC AAY95099;
 XX 30-JUN-2000 (first entry)
 DT Anti-gp120 antibody heavy chain variable region from clone b21.
 DE Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX Homo sapiens.
 XX AU9948756-A.
 XX 17-FEB-2000.
 PD
 FF 16-SEP-1999; 99AU-00048756.
 XX
 PR 16-SEP-1999; 99AU-00048756.
 XX (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-293393/26.
 DR Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX
 PS Example 9; Fig 10; 366pp; English.

The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the

CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV

XX Sequence 124 AA;

Query Match 81.8%; Score 649; DB 3; Length 124;
 Best Local Similarity 95.2%; Pred. No. 8.9e-55;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPMWGWINPYNGNKEFSAK 82
 Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPMWGWINPYNGNKEFSAK 60
 QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYTWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 24

AAR75606
 ID AAR75606 standard; protein; 124 AA.

XX AAR75606;

DT 11-MAR-1996 (first entry)

DE VH Fab H4H1-5 binds to gp120.

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy.

XX Synthetic.

Key	Location/Qualifiers
FT Region	1..27
FT Region	/label= FR1
FT Region	28..32
FT Region	/label= CDR1
FT Region	33..46
FT Region	/label= FR2
FT Region	47..63
FT Region	/label= CDR2
FT Region	64..95
FT Region	/label= FR3
FT Region	96..113
FT Region	/label= CDR3
FT Region	114..124
FT Region	/label= FR4

XX WO9511317-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011907.

XX 19-OCT-1993; 93US-00139409.

XX 26-APR-1994; 94US-00233619.

XX 19-SEP-1994; 94US-00308841.

XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Burton DR, Lerner RA;
 PI WPI; 1995-170235/22.
 DR Synthetic human neutralising monoclonal antibodies to human
 XX immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
 PT induced disease.
 XX Example 4B1; Fig 7; 249pp; English.

XX The sequences given in AAR75604-09 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
 CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
 CC sequences containing the preferred His residue as the first residue of
 CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
 CC used in the production of a human monoclonal antibody (Mab) which is
 CC capable of immunoreacting with, and neutralising HIV. The Mab's are
 CC capable of reducing HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of <100 ng of antibody per
 CC ml. They can be used to provide passive immunotherapy to HIV in a human.
 CC They neutralise HIV more effectively than antibodies selected from non-
 CC randomised combinatorial libraries

XX Sequence 124 AA;

Query Match 81.7%; Score 648; DB 2; Length 124;
 Best Local Similarity 96.8%; Pred. No. 1.1e-54;
 Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPMWGWINPYNGNKEFSAK 82
 Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPMWGWINPYNGNKEFSAK 60
 QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146

Db 121 IVSS 124

RESULT 25

AAR75609
 ID AAR75609 standard; protein; 124 AA.

XX AAR75609;

DT 11-MAR-1996 (first entry)

XX VH Fab H4H1-8 binds to gp120.

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy.

XX Synthetic.

Key	Location/Qualifiers
FT Region	1..27
FT Region	/label= FR1
FT Region	28..32
FT Region	/label= CDR1
FT Region	33..46
FT Region	/label= FR2
FT Region	47..63
FT Region	/label= CDR2
FT Region	64..95
FT Region	/label= FR3
FT Region	96..113

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FT FT /label= CDR3
FT FT 114..124
FT FT /label= FR4
XX XX
PN PN WO9511317-A1.
XX XX
PD PD 27-APR-1995.
XX XX
XX XX 19-OCT-1994; 94WO-US011907.
XX XX
XX XX 19-OCT-1993; 93US-00139409.
XX XX
PR PR 26-APR-1994; 94US-00233619.
XX XX
PR PR 19-SEP-1994; 94US-00308841.
XX XX
XX XX (SCRI ) SCRIPPS RES INST.
XX XX
XX XX Barbas CF, Burton DR, Lerner RA;
XX XX
XX XX WPI; 1995-170235/22.
XX XX
XX XX Synthetic human neutralising monoclonal antibodies to human
FT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
FT induced disease.
XX XX
XX XX Example 4B1; Fig 7; 249pp; English.
XX XX
XX XX The sequences given in AAR75570-09 represent human Fab's comprising
CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
CC sequences containing the preferred His residue as the first residue of
CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
CC used in the production of a human monoclonal antibody (MAB) which is
CC capable of immunoreacting with, and neutralising HIV. The MAB's are
CC capable of reducing HIV infectivity titre in an in vitro virus
CC infectivity assay by 50% at a concentration of <100 ng of antibody per
CC ml. They can be used to provide passive immunotherapy to HIV in a human.
CC They neutralise HIV more effectively than antibodies selected from non-
CC randomised combinatorial libraries
XX XX
XX XX Sequence 124 AA;
XX XX
XX XX Query Match 81.7%; Score 648; DB 2; Length 124;
XX XX Best Local Similarity 96.8%; Pred. No. 1.1e-54;
XX XX Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX XX 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGKFSK 82
XX XX 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGKFSK 60
XX XX
XX XX 83 FQDRVTFADTSANTATMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
XX XX 61 FQDRVTFADTSANTATMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
XX XX
XX XX 143 IVSS 146
XX XX 121 IVSS 124
XX XX
XX XX AAR75572 standard; protein; 124 AA.
XX XX
XX XX AAR75572;
XX XX
XX XX 05-MAR-1996 (first entry)
XX XX
XX XX VH Fab 3b9 binds to gp120.
XX XX
XX XX Human, Fab; variable chain; heavy; light; region: VH; VL; HIV; gp120;
XX XX 3b1; 3b3; 3b4; 3b9; M74; humanised; monoclonal antibody; MAB;
XX XX immunoreaction; neutralisation; passive immunotherapy.
XX XX
XX XX Synthetic.
XX XX

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XX XX Location/Qualifiers
FH Key
FT Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3
FT Region 114..124
FT /label= FR4
XX XX
XX XX WO9511317-A1.
XX XX
XX XX 27-APR-1995.
XX XX
XX XX 19-OCT-1994; 94WO-US011907.
XX XX
XX XX 19-OCT-1993; 93US-00139409.
XX XX
PR PR 26-APR-1994; 94US-00233619.
XX XX
PR PR 19-SEP-1994; 94US-00308841.
XX XX
XX XX (SCRI ) SCRIPPS RES INST.
XX XX
XX XX Barbas CF, Burton DR, Lerner RA;
XX XX
XX XX WPI; 1995-170235/22.
XX XX
XX XX Synthetic human neutralising monoclonal antibodies to human
PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
PT induced disease.
XX XX
XX XX Claim 6; Page 172-173; 249pp; English.
XX XX
XX XX The sequences given in AAR75568-72 represent human Fab's comprising
CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
CC have randomised amino acids in the entire CDR1 and in four of the 18
CC amino acid residues in CDR3. These Fab's are used in the production of a
CC human monoclonal antibody (MAB) which is capable of immunoreacting with,
CC and neutralising HIV. The MAB's are capable of reducing HIV infectivity
CC titre in an in vitro virus infectivity assay by 50% at a concentration of
CC <100 ng of antibody per ml. They can be used to provide passive
CC immunotherapy to HIV in a human. They neutralise HIV more effectively
CC than antibodies selected from non-randomised combinatorial libraries
XX XX
XX XX Sequence 124 AA;
XX XX
XX XX Query Match 81.5%; Score 646; DB 2; Length 124;
XX XX Best Local Similarity 95.2%; Pred. No. 1.7e-54;
XX XX Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX XX
XX XX 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGKFSK 82
XX XX 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGKFSK 60
XX XX
XX XX 83 FQDRVTFADTSANTATMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
XX XX 61 FQDRVTFADTSANTATMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
XX XX
XX XX 143 IVSS 146
XX XX 121 IVSS 124
XX XX
XX XX AAR75570 standard; protein; 124 AA.
XX XX
XX XX RESULT 27
XX XX AAR75570
XX XX ID AAR75570 standard; protein; 124 AA.

```

```

XX AAR75570;
AC 05-MAR-1996 (first entry)
XX
XX VH Fab 3b3 binds to gp120.
DE
XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; 3b9; M14; humanised; monoclonal antibody; MAB;
KW immunoreaction; neutralisation; passive immunotherapy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3
FT Region 114..124
FT /label= FR4
XX
XX WO9511317-A1.
PN
XX
XX 27-APR-1995.
PD
XX
XX 19-OCT-1994; 94WO-US011907.
PF
XX
XX 19-OCT-1993; 93US-00139409.
PR
XX 26-APR-1994; 94US-00233619.
PR
XX 19-SEP-1994; 94US-00308841.
PR
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX Barbas CF, Burton DR, Lerner RA;
XX
XX WPI; 1995-170235/22.
XX
XX Synthetic human neutralising monoclonal antibodies to human
PT immunodeficiency virus - used for diagnosis and immuno-therapy of HIV-
PT induced disease.
XX
XX Claim 6; Page 171; 249pp; English.
XX
XX The sequences given in AAR75568-72 represent human Fab's comprising
XX variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
XX 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as M14 but
XX have randomised amino acids in the entire CDR1 and in four of the 18
XX amino acid residues in CDR3. These Fab's are used in the production of a
XX human monoclonal antibody (MAB) which is capable of immunoreacting with,
XX and neutralising HIV. The MAB's are capable of reducing HIV infectivity
XX titre in an in vitro virus infectivity assay by 50% at a concentration of
XX <100 ng of antibody per ml. They can be used to provide passive
XX immunotherapy to HIV in a human. They neutralise HIV more effectively
XX than antibodies selected from non-randomised combinatorial libraries
XX
XX Sequence 124 AA;
XX
XX Query Match 81.3%; Score 645; DB 2; Length 124;
XX Best Local Similarity 95.2%; Pred. No. 2.2e-54;
XX Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX 23 LVQSGAEVKKPGASVKVSQCOAGSFRFSNFTVHWVROAPGQRFEMWGWINPYNKFEFSK 82
XX
XX 1 LEQSGAEVKKPGASVKVSQCOAGSFRFSNFTVHWVROAPGQRFEMWGWINPYNKFEFSK 60
XX

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QY 83 PQDRVTFPTADTSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYYMDVVGKGTTV 142
DB 61 PQDRVTFPTADTSANTAYMELRSLRSADTAVYICARVGEWDDSPQDNYYMDVVGKGTTV 120
QY 143 IVSS 146
DB 121 IVSS 124
XX
XX AAR54335 standard; protein; 124 AA.
XX
XX AAR54335;
AC
XX
XX 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin L12-HC12 shuffled heavy chain.
DE
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; heavy chain; shuffled;
KW variable region; framework; complementarity determining region.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 1..31
FT /label= FR1
FT Region 32..36
FT /label= CDR1
FT Region 37..50
FT /label= FR2
FT Region 51..67
FT /label= CDR2
FT Region 68..99
FT /label= FR3
FT Region 100..117
FT /label= CDR3
FT Region 118..124
FT /label= FR4
XX
XX WO9407922-A1.
XX
XX 14-APR-1994.
PD
XX
XX 30-SEP-1993; 93WO-US009328.
PF
XX
XX 30-SEP-1992; 92US-00954148.
PR
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX diagnosis and for passive immuno-therapy.
XX
XX Example; Page 206-207; 248pp; English.
XX
XX The anti-HIV gp120 light chain clone b12 (AAR54253) was recombined with a
XX heavy chain library to construct a new library L12-HCn. Ten heavy chains
XX which recombined with the b12 light chain and bound gp120 by panning were
XX chosen for sequence analysis. AAR54335 was one of these heavy chains.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 124 AA;
XX
XX Query Match 80.9%; Score 641.5; DB 2; Length 124;
XX Best Local Similarity 94.4%; Pred. No. 4.7e-54;
XX Matches 117; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
XX

```


CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
SQ Sequence 124 AA;

Query Match 80.9%; Score 641.5; DB 3; Length 124;
Best Local Similarity 94.4%; Pred. No. 4.7e-54;
Matches 117; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
QY 20 QVQLV-CSGAEVKKPGASVKVSQCSGYRFSNFIHWVRQAPGQRFPEWNGWINPYNGNKE 78
Db 1 QVKLLQCSGAEVKKPGASVKVSQCSGYRFSNFIHWVRQAPGQRFPEWNGWINPYNGNKE 50
QY 79 FSAKFQDRVTFTADTSANTAYMELSLRSADTAIYYCARVGPYSMDSDSPQDNYIMDVWGK 138
Db 61 FSAKPRDRVTFTADTDANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYIMDVWGK 120
QY 139 GTTV 142
Db 121 GTTV 124

Search completed: August 26, 2004, 13:37:45
Job time : 56.5333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:32:07 ; Search time 45.4667 Seconds
(without alignments)
770.584 Million cell updates/sec

Title: US-10-016-986-66
Perfect score: 674
Sequence: 1 LEQSGAEVKPGASVKVSCO.....PQDNYMDVWGKTTIVVSS 124

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	674	100.0	124	2	AAR54244 Anti-HIV
2	674	100.0	124	2	AAR75568 VH Fab MT
3	674	100.0	124	2	AAW01227 VH region
4	674	100.0	124	3	AAAY98206 Anti-gp12
5	674	100.0	124	3	AAAY95097 Anti-gp12
6	667	99.0	146	2	AAW01228 VH region
7	667	99.0	146	3	AAAY98285 Modified
8	667	99.0	146	3	AAAY95176 Modified
9	667	99.0	146	7	ADAE6734 Human IGG
10	667	99.0	476	7	ABRG1564 Human MAb
11	664	98.5	124	2	AAAR75604 VH Fab H4
12	663	98.4	124	2	AAAR75605 VH Fab H4
13	660	97.9	124	2	AAAR54245 Anti-HIV
14	660	97.9	124	3	AAW01246 VH region
15	660	97.9	124	3	AAAY98207 Anti-gp12
16	660	97.9	124	3	AAAY95098 Anti-gp12
17	657	97.5	124	2	AAAR75607 VH Fab H4
18	657	97.5	124	2	AAAR75608 VH Fab H4
19	656	97.3	124	2	AAAR54246 Anti-HIV
20	656	97.3	124	2	AAW01247 VH region
21	656	97.3	124	3	AAAY98208 Anti-gp12
22	656	97.3	124	3	AAAY95099 Anti-gp12
23	655	97.2	124	2	AAAR75606 VH Fab H4
24	655	97.2	124	2	AAAR75609 VH Fab H4
25	653	96.9	124	2	AAAR75572 VH Fab 3b

26	652	96.7	124	2	AAR75570	AAR75570 VH Fab 3b
27	652	96.7	250	3	AAAY44346	AAAY44346 3B3 anti-b
28	646	95.8	124	2	AAAR54335	AAAR54335 Anti-HIV
29	646	95.8	124	2	AAW01309	AAW01309 VH region
30	646	95.8	124	3	AAAY98270	AAAY98270 Anti-gp12
31	646	95.8	124	3	AAAY95161	AAAY95161 Anti-gp12
32	642	95.3	124	2	AAR75569	AAR75569 VH Fab 3b
33	629.5	93.4	123	2	AAR75571	AAR75571 VH Fab 3b
34	636	92.9	124	2	AAR75617	AAR75617 VH Fab M5
35	636	92.9	124	2	AAR75616	AAR75616 VH Fab M5
36	625	92.7	124	2	AAAR75615	AAAR75615 VH Fab M5
37	619	91.8	124	2	AAAR75610	AAAR75610 VH Fab M5
38	619	91.8	124	2	AAAR75613	AAAR75613 VH Fab M5
39	618	91.7	124	2	AAAR75611	AAAR75611 VH Fab M5
40	617	91.5	124	2	AAAR75612	AAAR75612 VH Fab M5
41	617	91.5	124	2	AAAR75614	AAAR75614 VH Fab M5
42	607	90.1	124	2	AAAR75640	AAAR75640 VH Fab H1
43	606	89.9	124	2	AAAR75638	AAAR75638 VH Fab H1
44	606	89.9	124	2	AAAR75641	AAAR75641 VH Fab H1
45	605	89.8	124	2	AAAR75639	AAAR75639 VH Fab H1
46	577	85.6	124	2	AAAR54331	AAAR54331 Anti-HIV
47	577	85.6	124	2	AAW01305	AAW01305 VH region
48	577	85.6	124	3	AAAY98266	AAAY98266 Anti-gp12
49	577	85.6	124	3	AAAY95157	AAAY95157 Anti-gp12
50	554	82.2	124	2	AAAR54330	AAAR54330 Anti-HIV
51	554	82.2	124	2	AAAR54336	AAAR54336 Anti-HIV
52	554	82.2	124	2	AAW01310	AAW01310 VH region
53	554	82.2	124	2	AAW01304	AAW01304 VH region
54	554	82.2	124	3	AAAY98271	AAAY98271 Anti-gp12
55	554	82.2	124	3	AAAY98265	AAAY98265 Anti-gp12
56	554	82.2	124	3	AAAY95156	AAAY95156 Anti-gp12
57	554	82.2	124	3	AAAY95162	AAAY95162 Anti-gp12
58	548	81.3	125	2	AAAR54333	AAAR54333 Anti-HIV
59	548	81.3	125	2	AAAR54268	AAAR54268 Anti-HIV
60	548	81.3	125	2	AAW01307	AAW01307 VH region
61	548	81.3	125	2	AAW01303	AAW01303 VH region
62	548	81.3	125	3	AAAY98264	AAAY98264 Anti-gp12
63	548	81.3	125	3	AAAY98268	AAAY98268 Anti-gp12
64	548	81.3	125	3	AAAY95159	AAAY95159 Anti-gp12
65	548	81.3	125	3	AAAY95155	AAAY95155 Anti-gp12
66	545	80.9	124	2	AAAR54332	AAAR54332 Anti-gp12
67	545	80.9	124	2	AAW01306	AAW01306 VH region
68	545	80.9	124	3	AAAY98267	AAAY98267 Anti-gp12
69	541	80.3	126	3	AAAY95158	AAAY95158 Anti-HIV
70	541	80.3	126	3	AAAY95152	AAAY95152 Anti-HIV
71	541	80.3	126	3	AAAY98263	AAAY98263 Anti-gp12
72	541	80.3	126	3	AAAY95154	AAAY95154 Anti-gp12
73	538	79.8	124	2	AAAR54269	AAAR54269 Anti-HIV
74	538	79.8	124	2	AAW01311	AAW01311 VH region
75	538	79.8	124	3	AAAY98272	AAAY98272 Anti-gp12
76	538	79.8	124	3	AAAY95163	AAAY95163 Anti-gp12
77	538	79.8	126	2	AAW01302	AAW01302 VH region
78	527	78.2	125	2	AAAR54334	AAAR54334 Anti-HIV
79	527	78.2	125	2	AAW01308	AAW01308 VH region
80	527	78.2	125	3	AAAY98269	AAAY98269 Anti-gp12
81	527	78.2	125	3	AAAY95160	AAAY95160 Anti-gp12
82	455.5	67.6	253	5	ABP45848	ABP45848 Human Bly
83	452.5	67.4	245	5	ABP45885	ABP45885 Human Bly
84	452.5	67.1	253	5	ABP45519	ABP45519 Human Bly
85	449.5	66.7	230	4	AAU08382	AAU08382 Anti-ORGb
86	449.5	66.7	230	4	AAU08383	AAU08383 Anti-ORGb
87	446.5	66.2	249	5	ABP45719	ABP45719 Human Bly
88	444	65.9	251	5	ABP45066	ABP45066 Human Bly
89	444	65.9	257	5	ABP45343	ABP45343 Human Bly
90	443	65.7	124	6	AAE37618	AAE37618 Chimpanze
91	442	65.6	127	6	ADA89122	ADA89122 MS-Pro-29
92	440.5	65.4	123	5	AAO18448	AAO18448 Anti-GD2
93	440.5	65.4	139	2	AAAR43689	AAAR43689 PSI.3/Hum
94	440.5	65.4	139	2	AAAR62678	AAAR62678 CY1746RHA
95	440.5	65.4	139	2	AAAR62679	AAAR62679 CY1746RHB
96	440	65.3	255	5	ABP45179	ABP45179 Human Bly
97	438	65.0	123	6	ABR55795	ABR55795 Heavy cha
98	438	65.0	251	5	ABP44949	ABP44949 Human Bly

99 438 65.0 252 5 ABP45943 Abp45943 Human Bly
100 437.5 64.9 251 5 ABP45910 Abp45910 Human Bly

ALIGNMENTS

RESULT 1
AAR54244 ID AAR54244 standard; protein; 124 AA.
XX AC AAR54244;
XX DT 25-MAR-2003 (revised)
XX DT 10-NOV-1994 (first entry)
XX DE Anti-HIV gp120 immunoglobulin heavy chain variable region b4.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; heavy chain; variable region;
KW framework region; complementarity determining region.
XX OS Homo sapiens.

Key	Location/Qualifiers
FT Region	1..27
FT Region	/label= FR1
FT Region	28..32
FT Region	/label= CDR1
FT Region	33..46
FT Region	/label= FR2
FT Region	47..63
FT Region	/label= CDR2
FT Region	64..95
FT Region	/label= FR3
FT Region	96..113
FT Region	/label= CDR3
FT Region	114..124
FT Region	/label= FR4
PN	WO9407922-A1.
PD	14-APR-1994.
PF	30-SEP-1993; 93WO-US009328.
PR	30-SEP-1992; 92US-00954148.
PA	(SCRI) SCRIPPS RES INST.
PI	Burton DR, Barbas CF, Lerner RA;
XX	WPI; 1994-135516/16.
XX	New human monoclonal antibodies neutralising HIV - react with gp120 or
PT	gp120 and nucleic acid encoding them, useful for in vivo or in vitro
PT	diagnosis and for passive immuno-therapy.
XX	Claim 1; Page 163-164; 248pp; English.
XX	Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC	using primers specific for heavy and light chain variable regions. The
CC	amplification products were inserted into a dicistronic vector to produce
CC	a library of fragments. E.coli Xli Blue cells were transformed with the
CC	library. Filamentous phage were produced which expressed the WAB regions
CC	on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC	immunoreactive clones. The heavy chain VH region sequence AAR54244
CC	neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
SQ	Sequence 124 AA;
Query Match	100.0%; Score 674; DB 2; Length 124;
Best Local Similarity	100.0%; Pred. No. 7.9e-61;

	Matches	124;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	LEQSGAEVKKPGASVKVSQ	ASGYRFSN	FVTHWVRQ	APGQRF	FMWGW	INPYN	GNKEFS	AK	60
Db	1	LEQSGAEVKKPGASVKVSQ	ASGYRFSN	FVTHWVRQ	APGQRF	FMWGW	INPYN	GNKEFS	AK	60
QY	61	FQDRVTFTADT	SANTAYMELRS	LSADTAVY	YCARVGP	YSWDDSP	QDNYM	YMDVWGK	TTV	120
Db	61	FQDRVTFTADT	SANTAYMELRS	LSADTAVY	YCARVGP	YSWDDSP	QDNYM	YMDVWGK	TTV	120
QY	121	IVSS	124							
Db	121	IVSS	124							

RESULT 2
AAR75568 ID AAR75568 standard; protein; 124 AA.

XX AC AAR75568;
XX DT 05-MAR-1996 (first entry)
XX DE VH Fab MT4 binds to gp120.
XX KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
KW immunoreaction; neutralisation; passive immunotherapy.

Key	Location/Qualifiers
FT Region	1..27
FT Region	/label= FR1
FT Region	28..32
FT Region	/label= CDR1
FT Region	33..46
FT Region	/label= FR2
FT Region	47..63
FT Region	/label= CDR2
FT Region	64..95
FT Region	/label= FR3
FT Region	96..113
FT Region	/label= CDR3
FT Region	114..124
FT Region	/label= FR4

WO95111317-A1.

XX 27-APR-1995;
XX 19-OCT-1994; 94WO-US011907.
XX 19-OCT-1993; 93US-00139409.
XX 26-APR-1994; 94US-00233619.
XX 19-SEP-1994; 94US-00308841.
XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1995-170235/22.
XX N-PSDB; AAQ92540.

XX Synthetic human neutralising monoclonal antibodies to human
PT immunodeficiency virus - used for diagnosis and immuno-therapy of HIV-
PT induced disease.
XX Claim 9; Page 170; 249pp; English.

XX The sequences given in AAR75568-72 represent human Fab's comprising
CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as Mt4 but

CC have randomised amino acids in the entire CDR1 and in four of the 18
 CC amino acid residues in CDR3. These Fab's are used in the production of a
 CC human monoclonal antibody (Mab) which is capable of immunoreacting with,
 CC and neutralising HIV. The Mab's are capable of reducing HIV infectivity
 CC titre in an in vitro virus infectivity assay by 50% at a concentration of
 CC <100 ng of antibody per ml. They can be used to provide passive
 CC immunotherapy to HIV in a human. They neutralise HIV more effectively
 CC than antibodies selected from non-randomised combinatorial libraries
 XX
 SQ Sequence 124 AA;

Query Match 100.0%; Score 674; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.9e-61;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFEFSK 60

QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 3

AAW01227
 ID AAW01227 standard; protein; 124 AA.

XX AC AAW01227;

XX DT 27-JAN-1997 (first entry)

XX DE VH region of HIV neutralising Mab, clones b4 and b12.
 XX HV chain; light chain; variable region; VH; monoclonal antibody; Mab;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4

XX WO9602273-A1.

XX PD 01-FEB-1996.

XX PF 11-JUL-1995; 95WO-US008743.

XX PR 18-JUL-1994; 94US-00276952.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Burton DR, Barbas CF, Lerner RA;

XX

DR WPI; 1996-179601/18.

XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.

PS Claim 9; Fig 10; 366pp; English.

XX This sequence represents the heavy chain variable region (VH) of a
 CC monoclonal antibody (Mab) which is immunoreactive with HIV glycoprotein
 CC gp120 and is capable of neutralising HIV. This sequence represents the
 CC sequence of clones b4 and b12. The Mab has the capacity to reduce HIV
 CC infectivity titre in an in vivo virus infectivity assay by 50% at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. This sequence forms the heavy
 CC chain component of Mab's with the light chain sequences given in
 CC AAW01273, AAW01275-76, AAW01293, AAW01296, and AAW01299-300. The Mab may
 CC be used for determining immunocompetence of a human anti-HIV antibody and
 CC in the detection of HIV infection

SQ Sequence 124 AA;

Query Match 100.0%; Score 674; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.9e-61;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFEFSK 60

QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 4

AA98206
 ID AA98206 standard; protein; 124 AA.

XX AC AA98206;

XX DT 04-JUL-2000 (first entry)

XX DE Anti-Gp120 antibody heavy chain variable region from clone b4.

XX KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.

XX OS Homo sapiens.

XX PN AU9948754-A.

XX PD 17-FEB-2000.

XX PF 16-SEP-1999; 99AU-00048754.

XX PR 16-SEP-1999; 99AU-00048754.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Burton DR, Barbas CF, Lerner RA;

XX DR WPI; 2000-246867/22.

XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.

XX

Claim 1; Fig 10; 374pp; English.

This sequence represents a fragment of the antibodies of the invention. The invention relates to the production of an anti-HIV (human immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 70 ng/ml. The method for the production of the antibody comprises: (a) providing a first polynucleotide encoding a heavy chain immunoglobulin amino acid sequence (which does not comprise the sequence represented by AAY98206) and a second polynucleotide encoding a light chain immunoglobulin amino acid sequence; (b) inserting the first and second polynucleotide sequences into a host cell; (c) maintaining the host cell in conditions which allow the amino acid sequences encoded by the polynucleotides to be expressed in the host cell; and (d) isolating the antibody comprising the heavy and light chain immunoglobulin amino acid sequences from the host cell. The anti-HIV gp-120 monoclonal antibody is used for providing passive immunotherapy to HIV in a human. They can be administered to high-risk patients to reduce the likelihood and/or severity of HIV-induced disease and to patients who are already HIV-infected. The antibodies are used for neutralising field isolates which provides information about the immunocompetence of an immune response in HIV patients, for detecting HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for producing anti-idiotypic antibodies which can be used for active immunisation and to screen human monoclonal antibodies to identify those with the same binding specificity and to monitor the course of HIV disease therapy by measuring the changes in concentration of HIV present in the body or in body fluids by immunoassay. The anti-HIV gp-120 monoclonal antibodies are encoded by a human polynucleotide sequence and when used in vivo for diagnosis and immunotherapy of HIV-induced disease reduce the problems of significant host immune response to the antibodies associated with monoclonal antibodies of xenogenic or chimeric derivation. Note: The present sequence is specifically not claimed

Sequence 124 AA;

Query Match 100.0%; Score 674; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFQFWGWIHPYNGKFSK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFQFWGWIHPYNGKFSK 60

QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124
DB 121 IVSS 124

RESULT 5

AA95097
ID AAY95097 standard; protein; 124 AA.

AC AA95097;

DT 30-JUN-2000 (first entry)

DE Anti-gp120 antibody heavy chain variable region from clone b4.

KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS Homo sapiens.

FN AU9948756-A.

PD 17-FEB-2000.

XX

PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-293393/26.
XX
PT Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
XX
PS Example 9; Fig 10; 366pp; English.

The present sequence represents a fragment of an anti-human immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV mature glycoprotein gp120 preferentially over HIV precursor glycoprotein gp160 and neutralises HIV and which reduces HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 700 ng/ml. The antibodies are used as reagents for the diagnosis and immunotherapy of HIV induced disease. They are useful as neutralising field isolates and provide useful information regarding the immunocompetence of an immune response in HIV infected patients. The monoclonal antibodies are useful for producing anti-idiotypic antibodies which can be used to screen human monoclonal antibodies to identify whether the antibody has the same binding specificity as the antibodies of the invention. The neutralising antibodies define new epitopes on the HIV gp120 and gp41 glycoproteins, thus increasing the availability of new immunotherapeutic human monoclonal antibodies. A major advantage of the monoclonal antibodies derives from the fact that they are encoded by a human polynucleotide sequence. Thus in vivo use of the monoclonal antibodies for diagnosis and immunotherapy of HIV induced disease greatly reduces the problems of significant host immune response to the passively administered antibodies which is a problem commonly encountered when monoclonal antibodies of xenogenic or chimeric derivation are utilized. An additional major advantage of the monoclonal antibodies described derives from the fact that they immunoreact with a unique determinant present on mature HIV glycoprotein gp120. This class of antibodies is particularly effective at neutralising field isolates of HIV

Sequence 124 AA;

Query Match 100.0%; Score 674; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFQFWGWIHPYNGKFSK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFQFWGWIHPYNGKFSK 60

QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124
DB 121 IVSS 124

RESULT 6

AAW01228
ID AAW01228 standard; protein; 146 AA.

XX AAW01228;

XX 16-OCT-2003 (revised)

DT 27-JAN-1997 (first entry)

XX VH region of HIV neutralising Mab, IgG1 b12.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;

KW

KW	HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW	virus infectivity assay; precursor gp160; immunocompetence; human;
KW	anti-HIV antibody; detection; HIV infection.
XX	
OS	Homo sapiens.
OS	Mus musculus.
OS	Chimeric.
XX	
FH	Key
FT	Peptide
FT	1. .20
FT	/note= "Mouse B72.3 heavy chain leader sequence"
FT	Peptide
FT	21. .26
FT	/note= "Human VH consensus sequence"
FT	Protein
FT	27. .146
FT	/note= "Human Fab b12"
XX	
PN	W09602273-A1.
XX	
PD	01-FEB-1996.
XX	
XX	11-JUL-1995; 95WO-US008743.
XX	
PR	18-JUL-1994; 94US-00276852.
XX	
XX	(SCRI) SCRIPPS RES INST.
XX	
PI	Burton DR, Barbas CP, Lerner RA;
XX	
DR	WPI; 1996-179601/18.
DR	N-PSDB; AAT40914.
XX	
PT	Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT	immuno:therapy and detection of HIV infection.
XX	
PS	Claim 10; Page 275-276; 366pp; English.
XX	
CC	This sequence represents the heavy chain variable region (VH) of a
CC	monoclonal antibody (MAB) which is immunoreactive with HIV glycoprotein
CC	gp120 and is capable of neutralising HIV. This sequence contains the
CC	leader sequence derived from the mouse B72.3 heavy chain, and the human
CC	VH consensus sequence attached to the N-terminal of the b12 VH sequence.
CC	The DNA sequence contains a Kozak sequence for the control of VH
CC	expression. This sequence was amplified using the primer sequences given
CC	in AAT40889-92. A MAB containing this VH sequence has the capacity to
CC	reduce HIV infectivity titre in an in vivo virus infectivity assay by 50
CC	% at a concentration of less than 700 ng of antibody/ml, and binds mature
CC	gp120 preferentially over the precursor gp160. The MAB may be used for
CC	determining immunocompetence of a human anti-HIV antibody and in the
CC	detection of HIV infection. (Updated on 16-OCT-2003 to standardise OS
CC	field)
XX	
SQ	Sequence 146 AA;
	Query Match 99.0%; Score 667; DB 2; Length 146;
	Best Local Similarity 99.2%; Pred. No. 4.9e-60;
	Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	1 LQSGAEVKKPGASVKVSQASGYRFSNFIHWYRQAPGQRFEMWGWINPYNGNKEFSK 60
Db	23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWYRQAPGQRFEMWGWINPYNGNKEFSK 82
QY	61 FQDRVTFETADTSANTAYNMLSLSSADTANYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db	83 FQDRVTFETADTSANTAYNMLSLSSADTANYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY	121 IVSS 124
Db	143 IVSS 146
RESULT 7	
AAV98265	
ID	AAV98265 standard; protein; 146 AA.

Db	23	LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRF	FWGWINPYNKGFSAK	82
Qy	61	FQDRVTFADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYNDVWGKGT	TVV	120
Db	83	FQDRVTFADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYNDVWGKGT	TVV	142
Qy	121	IVSS	124	
Db	143	IVSS	146	
RESULT 8				
AAV95176				
ID	AAV95176	standard; protein; 146 AA.		
XX	AC			
XX	AC	AAV95176;		
XX	DT	30-JUN-2000 (first entry)		
XX	DE	Modified heavy chain variable region amino acid sequence.		
XX	KW	Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;		
XX	KW	reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;		
XX	KW	glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.		
XX	OS	Synthetic.		
XX	XX			
XX	PN	AU9948756-A.		
XX	PD	17-FEB-2000.		
XX	PF	16-SEP-1999; 99AU-00048756.		
XX	PR	16-SEP-1999; 99AU-00048756.		
XX	PA	(SCRI) SCRIPPS RES INST.		
XX	PI	Burton DR, Barbas CF, Lerner RA;		
XX	XX	WPI; 2000-293393/26.		
XX	PT	Novel human monoclonal antibodies which immunoreact with and neutralize		
XX	PT	human immunodeficiency virus useful for treating HIV infections.		
XX	PS	Example 4; Page 111; 366pp; English.		
XX	CC	The present sequence represents a fragment of an anti-human		
XX	CC	immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to		
XX	CC	a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV		
XX	CC	mature glycoprotein gp120 preferentially over HIV precursor glycoprotein		
XX	CC	gp160 and neutralises HIV and which reduces HIV infectivity titre in an		
XX	CC	in vitro virus infectivity assay by 50%, at a concentration of less than		
XX	CC	700 ng/ml. The antibodies are used as reagents for the diagnosis and		
XX	CC	immunotherapy of HIV induced disease. They are useful as neutralising		
XX	CC	field isolates and provide useful information regarding the		
XX	CC	immunocompetence of an immune response in HIV infected patients. The		
XX	CC	monoclonal antibodies are useful for producing anti-idiotypic antibodies		
XX	CC	which can be used to screen human monoclonal antibodies to identify		
XX	CC	whether the antibody has the same binding specificity as the antibodies		
XX	CC	of the invention. The neutralising antibodies define new epitopes on the		
XX	CC	HIV gp120 and gp41 glycoproteins, thus increasing the availability of new		
XX	CC	immunotherapeutic human monoclonal antibodies. A major advantage of the		
XX	CC	monoclonal antibodies derives from the fact that they are encoded by a		
XX	CC	human polynucleotide sequence. Thus in vivo use of the monoclonal		
XX	CC	antibodies for diagnosis and immunotherapy of HIV induced disease greatly		
XX	CC	reduces the problems of significant host immune response to the passively		
XX	CC	administered antibodies which is a problem commonly encountered when		
XX	CC	monoclonal antibodies of xenogeneic or chimeric derivation are utilized.		
XX	CC	An additional major advantage of the monoclonal antibodies described		
XX	CC	derives from the fact that they immunoreact with a unique determinant		
XX	CC	present on mature HIV glycoprotein gp120. This class of antibodies is		
XX	CC	particularly effective at neutralising field isolates of HIV		

polypeptide from which the motif is derived, where the resulting hybrid polypeptide binds with greater affinity to a disease causing or infectious conformer of the polypeptide that is the source of the polypeptide motif compared to a benign form of the polypeptide. Also described: (1) a nucleic acid molecule encoding (1); (2) a vector comprising the nucleic acid molecule; (3) a cell comprising the vector; (4) detecting an isoform or a prpsc form of a prion polypeptide or a polypeptide associated with a disease of protein aggregation, in a sample; (5) a solid support comprising a plurality of polypeptides described above; (6) detecting cells that contain a protein conformer associated with a disease of protein aggregation; (7) preparing a hybrid molecule that specifically interacts with one conformer of a protein involved in the disease mentioned above; and (8) an anti-idiotypic antibody that specifically binds to an infectious form of a prion protein. (I) has neuroprotective, neurotropic, antidiabetic, anticonvulsant, cerebroprotective, antiparkinsonian, cytostatic, nephrotropic, cardiant, antiinflammatory and antiarteriosclerotic activities, and can be used in gene therapy. The composition and methods of the present invention can be used in diagnosing or treating diseases of protein aggregation or conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine spongiform encephalopathy, Alzheimer's disease, Type II diabetes, Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis associated with chronic inflammatory disease, hereditary systemic amyloidosis associated with autosomal dominant inheritance of variant transthyretin gene, amyotrophic lateral sclerosis, Pick's disease, Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma of thyroid, chronic renal failure, congestive heart failure, senile cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis or familial amyloidosis. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 146 AA;

Query March 99.0%; Score 667; DB 7; Length 146;
Best Local Similarity 99.2%; Pred. No. 4.9e-60;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQCAAGYRFSNFIHWVROAPGQRFEMWGMINPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQCAAGYRFSNFIHWVROAPGQRFEMWGMINPYNGNKEFSK 82
QY 61 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY 121 IVSS 124
DB 143 IVSS 146

RESULT 10
ABR61564

ID ABR61564 standard; protein; 476 AA.

XX ABR61564;
XX ABR61564;
XX 15-JAN-2004 (first entry)
XX Human MAb IgG1b12 heavy chain.
XX Adeno-associated virus; rAAV; IgG1b12; ScFvX5; anti-HIV; antibacterial;
KW antirheumatic; antiarthritic; cytostatic; sedative; antiinflammatory;
KW neuroprotective; gene therapy; vaccine; antibody; MAb.
OS Homo sapiens.
XX WO2003087324-A2.
PN 23-OCT-2003.
XX 09-APR-2003; 2003WO-US010865.

PR 09-APR-2002; 2002US-0371501P.
XX (CHIL-) CHILDRENS HOSPITAL INC.
PA Clark KR, Johnson PR;
PI WPI; 2003-833721/77.
XX N-PSDB; ACF58045.
XX New recombinant adeno-associated virus (rAAV)/IgG1b12 or rAAV/ScFvX5
PT Genome, useful for preventing or treating viral infections (e.g. HIV),
PT bacterial infections or other chronic disease states (e.g. cancer,
PT inflammation or kuru).
XX Example 1; Page 35-37; Opp; English.

XX The invention relates to a recombinant adeno-associated virus (rAAV)/
CC IgG1b12 or rAAV/ScFvX5 genome. The rAAV is useful for gene delivery,
CC particularly in delivering antibody genes to target cells in mammals. The
CC antibodies may be used to prevent and/or treat viral infections
CC (particularly HIV), bacterial infections and other chronic disease states
CC (e.g. cancer, rheumatoid arthritis, inflammation, fatal familial
CC insomnia, kuru, Mad Cow Disease or Alpers syndrome). The present sequence
CC represents the human monoclonal antibody (MAb) IgG1b12 heavy chain
XX Sequence 476 AA;

Query March 99.0%; Score 667; DB 7; Length 476;
Best Local Similarity 99.2%; Pred. No. 1.9e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQCAAGYRFSNFIHWVROAPGQRFEMWGMINPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQCAAGYRFSNFIHWVROAPGQRFEMWGMINPYNGNKEFSK 82
QY 61 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY 121 IVSS 124
DB 143 IVSS 146

RESULT 11
AAR75604

ID AAR75604 standard; protein; 124 AA.

XX AAR75604;
XX 11-MAR-1996 (first entry)
XX VH Fab H4H1-1 binds to gp120.
DE Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; MT4; humanised; monoclonal antibody; MAb;
KW immunoreaction; neutralisation; passive immunotherapy.

OS Synthetic.

XX Key Location/Qualifiers
FH Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3

XX OS

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XX AAR54245;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 10-NOV-1994 (first entry)
XX DE
XX DB Anti-HIV gp120 immunoglobulin heavy chain variable region b7.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX KW neutralisation; monoclonal antibody; heavy chain; variable region;
XX KW framework region; complementarity determining region.
XX OS Homo sapiens.
XX FH
XX FT Location/Qualifiers
XX FT 1. .27
XX FT /label= FR1
XX FT 28. .32
XX FT /label= CDR1
XX FT 33. .46
XX FT /label= FR2
XX FT 47. .63
XX FT /label= CDR2
XX FT 64. .95
XX FT /label= FR3
XX FT 96. .113
XX FT /label= CDR3
XX FT 114. .124
XX FT /label= FR4
XX PN WO9407922-A1.
XX XX
XX PD 14-APR-1994.
XX PF 30-SEP-1993; 93WO-US009328.
XX PR 30-SEP-1992; 92US-00954148.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX PF 1994-135516/16.
XX DR
XX FT New human monoclonal antibodies neutralising HIV - react with gp120 or
XX FT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX FT diagnosis and for passive immuno-therapy.
XX PS Claim 1; Page 164; 248pp; English.
XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX CC using primers specific for heavy and light chain variable regions. The
XX CC amplification products were inserted into a dicistronic vector to produce
XX CC a library of fragments. E.coli XL1 Blue cells were transformed with the
XX CC library. Filamentous phage were produced which expressed the MAB regions
XX CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX CC immunoreactive clones. The heavy chain VH region sequence AAR54245
XX CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 124 AA;
XX
XX Query Match 97.9%; Score 660; DB 2; Length 124;
XX Best Local Similarity 96.8%; Pred. No. 2.1e-59;
XX Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWROAPQGRFEWGWINPYNNGNKEFSAK 60
XX DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWROAPQGRFEWGWINPYNNGNKEFSAK 60
XX
XX 61 FQDRVTFDTADTANTAYMEILSRSDATVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
XX DB 61 FQDRVTFDTADTANTAYMEILSRSDATVYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120

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OY 121 IVSS 124
DB 121 IVSS 124

RESULT 14
AAW01246
ID AAW01246 standard; protein; 124 AA.
XX AC AAW01246;
XX DT 28-JAN-1997 (first entry)
XX DE VH region of HIV neutralising MAB, IgG1 b7.
XX KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB;
XX KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX KW virus infectivity assay; precursor gp160; immunocompetence; human;
XX OS anti-HIV antibody; detection; HIV infection.
XX OS Homo sapiens.
XX FH
XX FT Location/Qualifiers
XX FT 1. .27
XX FT /label= FR1
XX FT 28. .32
XX FT /label= CDR1
XX FT 33. .46
XX FT /label= FR2
XX FT 47. .63
XX FT /label= CDR2
XX FT 64. .95
XX FT /label= FR3
XX FT 96. .113
XX FT /label= CDR3
XX FT 114. .124
XX FT /label= FR4
XX PN WO9602273-A1.
XX XX
XX PD 01-FEB-1996.
XX PF 11-JUL-1995; 95WO-US008743.
XX PR 18-JUL-1994; 94US-00276852.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX PF 1996-179601/18.
XX DR Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
XX FT immuno-therapy and detection of HIV infection.
XX PS Example; Fig 10; 366pp; English.
XX CC The sequences given in AAW01233-60 represent the heavy chain variable
XX CC regions (VH) of a series of monoclonal antibodies (MAB's) which are
XX CC immunoreactive with HIV glycoprotein gp120 and are capable of
XX CC neutralising HIV. This sequence represents the sequence of the JH6 gene
XX CC clone, b7. A MAB containing this VH sequence has the capacity to reduce
XX CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
XX CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
XX CC preferentially over the precursor gp160. The MAB may be used for
XX CC determining immunocompetence of a human anti-HIV antibody and in the
XX CC detection of HIV infection
XX SQ Sequence 124 AA;
XX
XX Query Match 97.9%; Score 660; DB 2; Length 124;
XX Best Local Similarity 96.8%; Pred. No. 2.1e-59;
XX Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Thu Aug 26 14:28:11 2004

CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
SQ Sequence 124 AA;
Query Match 97.9%; Score 660; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 2.1e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
DB 61 FQDRVTFTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 16
AA95098
ID AAY95098 standard; protein; 124 AA.
XX
AC AAY95098;
XX
DT 30-JUN-2000 (first entry)
XX
DE Anti-gp120 antibody heavy chain variable region from clone b7.
XX
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN AU9948756-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 2000-293393/26.
XX Novel human monoclonal antibodies which immunoreact with and neutralize
XX human immunodeficiency virus useful for treating HIV infections.
XX Example 9; Fig 10; 366pp; English.
XX The present sequence represents a fragment of an anti-human
XX immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
XX a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
XX mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
XX gp160 and neutralises HIV and which reduces HIV infectivity titre in an
XX in vitro virus infectivity assay by 50%, at a concentration of less than
XX 700 ng/ml. The antibodies are used as reagents for the diagnosis and
XX immunotherapy of HIV induced disease. They are useful as neutralising
XX field isolates and provide useful information regarding the

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFEMWGWINPYNKKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
DB 61 FQDRVTFTADTSANTAYMELRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 15
AA98207
ID AAY98207 standard; protein; 124 AA.
XX
AC AAY98207;
XX
DT 04-JUL-2000 (first entry)
XX
DE Anti-gp120 antibody heavy chain variable region from clone b7.
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
PN AU9948754-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048754.
XX
PR 16-SEP-1999; 99AU-00048754.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 2000-246867/22.
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX Example 9; Fig 10; 374pp; English.
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX (which does not comprise the sequence represented by AAY98206) and a
XX second polynucleotide encoding a light chain immunoglobulin amino acid
XX sequence; (b) inserting the first and second polynucleotide sequences
XX into a host cell; (c) maintaining the host cell in conditions which allow
XX the amino acid sequences encoded by the polynucleotides to be expressed
XX in the host cell; and (d) isolating the antibody comprising the heavy and
XX light chain immunoglobulin amino acid sequences from the host cell. The
XX anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used for
XX neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting HIV
XX in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active

CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 SQ Sequence 124 AA;

Query Match 97.8%; Score 660; DB 3; Length 124;
 Best Local Similarity 96.8%; Pred. No. 2.1e-59;
 Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFPEWGMWINPYNGNKEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFPEWGMWINPYNGNKEFSK 60
 QY 61 FQDRVTFADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGT 120
 DB 61 FQDRVTFADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGT 120
 QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 17
 AAR75607
 ID AAR75607 standard; protein; 124 AA.
 AC AAR75607;
 XX
 XX 11-MAR-1996 (first entry)
 DT VH Fab H4H1-6 binds to gp120.
 DE Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX
 OS Synthetic.

Key	Location/Qualifiers
FT Region	1..27
FT Region	/label= FR1
FT Region	28..32
FT Region	/label= CDR1
FT Region	33..46
FT Region	/label= FR2
FT Region	47..63
FT Region	/label= CDR2
FT Region	64..95
FT Region	/label= FR3
FT Region	96..113
FT Region	/label= CDR3
FT Region	114..124
FT Region	/label= FR4

XX WO9511317-A1.
 XX
 XX 27-APR-1995.
 PD
 XX

PF 19-OCT-1994; 94WO-US011907.
 XX
 PR 19-OCT-1993; 93US-00139409.
 PR 26-APR-1994; 94US-00233619.
 PR 19-SEP-1994; 94US-00306841.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Burton DR, Lerner RA;
 XX WPI; 1995-170235/22.
 DR
 XX Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
 PT induced disease.
 XX
 PS Example 4B1; Fig 7; 249pp; English.
 XX
 CC The sequences given in AAR75604-09 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
 CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
 CC sequences containing the preferred His residue as the first residue of
 CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
 CC used in the production of a human monoclonal antibody (Mab) which is
 CC capable of immunoreacting with, and neutralising HIV. The Mab's are
 CC capable of reducing HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of <100 ng of antibody per
 CC ml. They can be used to provide passive immunotherapy to HIV in a human.
 CC They neutralise HIV more effectively than antibodies selected from non-
 CC randomised combinatorial libraries
 XX
 SQ Sequence 124 AA;

Query Match 97.5%; Score 657; DB 2; Length 124;
 Best Local Similarity 96.8%; Pred. No. 4.3e-59;
 Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFPEWGMWINPYNGNKEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFPEWGMWINPYNGNKEFSK 60
 QY 61 FQDRVTFADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGT 120
 DB 61 FQDRVTFADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGT 120
 QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 18
 AAR75608
 ID AAR75608 standard; protein; 124 AA.
 AC AAR75608;
 XX
 XX 11-MAR-1996 (first entry)
 DT VH Fab H4H1-7 binds to gp120.
 DE Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX
 OS Synthetic.

Key	Location/Qualifiers
FT Region	1..27
FT Region	/label= FR1
FT Region	28..32
FT Region	/label= CDR1
FT Region	33..46
FT Region	/label= FR2

ID AAW01247 standard; protein; 124 AA.
XX AAW01247;
AC
XX 28-JAN-1997 (first entry)
DT
XX VH region of HIV neutralising MAb, IgG1 b21.
DE
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3
FT Region 114..124
FT /label= FR4
XX WO9602273-A1.
PN
XX 01-FEB-1996.
PD
XX 11-JUL-1995; 95WO-US008743.
PF
XX 18-JUL-1994; 94US-00276852.
PR
XX (SCRI) SCRIPPS RES INST.
PA
XX Burton DR, Barbas CF, Lerner RA;
PI
XX WPI; 1996-179601/18.
DR
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT immuno:therapy and detection of HIV infection.
PT
XX Example; Fig 10; 366pp; English.
PS
XX The sequences given in AAW01233-60 represent the heavy chain variable
CC regions (VH) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JH6 gene
CC clone, b21. A MAB containing this VH sequence has the capacity to reduce
CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
CC preferentially over the precursor gp160. The MAB may be used for
CC determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
XX
XX Sequence 124 AA;
SQ
Query Match 97.3%; Score 656; DB 2; Length 124;
Best Local Similarity 96.0%; Pred. No. 5.4e-59;
Matches 119; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
|||||
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
|||||
QY 61 FQDRVTFDTADTSANTAYMELRSLRSTDTAIYCARVGPGYTWDDSPQDNYYMDVWGKGTKV 120
|||||

Db 61 FQDRVTFDTADTSANTAYMELRSLRSTDTAIYCARVGPGYTWDDSPQDNYYMDVWGKGTKV 120
QY 121 IVSS 124
|||
Db 121 IVSS 124
RESULT 21
AA98208
ID AA98208 standard; protein; 124 AA.
XX AC AA98208;
XX DT 04-JUL-2000 (first entry)
XX DE Anti-gp120 antibody heavy chain variable region from clone b21.
XX KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX AU9948754-A.
PN
XX 17-FEB-2000.
PD
XX 16-SEP-1999; 99AU-00048754.
PF
XX 16-SEP-1999; 99AU-00048754.
PR
XX (SCRI) SCRIPPS RES INST.
PA
PI Burton DR, Barbas CF, Lerner RA;
XX WPI; 2000-246867/22.
DR
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
PT (HIV) used for providing passive immunotherapy to HIV are specific for
PT glycoprotein-120.
PT
XX Example 9; Fig 10; 374pp; English.
PS
XX This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
CC of reducing an HIV infectivity titre in an in vitro virus infectivity
CC assay by 50% at a concentration of less than 70 ng/ml. the method for the
CC production of the antibody comprises: (a) providing a first
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
CC (which does not comprise the sequence represented by AA98206) and a
CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies

CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation

SQ Sequence 124 AA;

Query Match 97.3%; Score 656; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 5.4e-59;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60
 Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60

QY 61 FQDRVTFPTADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
 Db 61 FQDRVTFPTADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124

Db 121 IVSS 124

RESULT 22

AA95099 ID AAY95099 standard; protein; 124 AA.

AC AAY95099;

DT 30-JUN-2000 (first entry)

DE Anti-gp120 antibody heavy chain variable region from clone b21.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

XX Homo sapiens.

XX AU9948756-A.

XX 17-FEB-2000.

XX 16-SEP-1999; 99AU-00048756.

XX 16-SEP-1999; 99AU-00048756.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 2000-293393/26.

XX Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.

XX Example 9; Fig 10; 366pp; English.

XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantages of the

CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV

XX Sequence 124 AA;

Query Match 97.3%; Score 656; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 5.4e-59;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60

Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKFSK 60

QY 61 FQDRVTFPTADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120

Db 61 FQDRVTFPTADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124

Db 121 IVSS 124

RESULT 23

AA975606 ID AAR75606 standard; protein; 124 AA.

AC AAR75606;

DT 11-MAR-1996 (first entry)

XX VH Fab H4H1-5 binds to gp120.

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b5; MT4; humanised; monoclonal antibody; MAb;
 KW immunoreaction; neutralisation; passive immunotherapy.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 1..27

FT /label= FR1

FT Region 28..32

FT /label= CDR1

FT Region 33..46

FT /label= FR2

FT Region 47..63

FT /label= CDR2

FT Region 64..95

FT /label= FR3

FT Region 96..113

FT /label= CDR3

FT Region 114..124

FT /label= FR4

XX WO9511317-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011907.

XX 19-OCT-1993; 93US-00139409.

XX 26-APR-1994; 94US-00233619.

XX 19-SEP-1994; 94US-00308841.

XX (SCRI) SCRIPPS RES INST.

```
XX PI Barbas CF, Burton DR, Lerner RA;
XX DR WPI; 1995-170235/22.
XX PT Synthetic human neutralising monoclonal antibodies to human
XX PT immunodeficiency virus - used for diagnosis and immunotherapy of HIV-
XX PT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX CC The sequences given in AAR75604-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (Mab) which is
XX CC capable of immunoreacting with, and neutralising HIV. The Mab's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SQ Sequence 124 AA;
XX Query Match 97.2%; Score 655; DB 2; Length 124;
XX Best Local Similarity 97.6%; Pred. No. 6.8e-59;
XX Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
QY 61 FQDRVTFDTATSANTAYMELRLSRASDTAVYYCARVGPVSWDDSPQDNYMDVWGKGTIV 120
DB 61 FQDRVTFDTATSANTAYMELRLSRASDTAVYYCARVGPVSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 24
AAR75609
ID AAR75609 standard; protein; 124 AA.
XX AAR75609;
XX DT 11-MAR-1996 (first entry)
XX DE VH Fab H4H1-8 binds to gp120.
XX KW Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
XX KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
XX KW immunoreaction; neutralisation; passive immunotherapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Region 1..27
FT FT /label= FR1
FT FT 28..32
FT FT /label= CDR1
FT FT 33..46
FT FT /label= FR2
FT FT 47..63
FT FT /label= CDR2
FT FT 64..95
FT FT /label= FR3
FT FT 96..113
FT FT /label= CDR3
FT FT 114..124
```

```
FT XX /label= FR4
PN XX WO9511317-A1.
XX XX
PD XX 27-APR-1995.
XX XX
PF 19-OCT-1994; 94WO-US011907.
XX XX
PR 19-OCT-1993; 93US-00139409.
PR 26-APR-1994; 94US-00233619.
PR 19-SEP-1994; 94US-00308841.
XX (SCRI ) SCRIPPS RES INST.
XX Barbas CF, Burton DR, Lerner RA;
PI WPI; 1995-170235/22.
XX DR
XX PT Synthetic human neutralising monoclonal antibodies to human
XX PT immunodeficiency virus - used for diagnosis and immunotherapy of HIV-
XX PT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX CC The sequences given in AAR75604-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (Mab) which is
XX CC capable of immunoreacting with, and neutralising HIV. The Mab's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SQ Sequence 124 AA;
XX Query Match 97.2%; Score 655; DB 2; Length 124;
XX Best Local Similarity 97.6%; Pred. No. 6.8e-59;
XX Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
QY 61 FQDRVTFDTATSANTAYMELRLSRASDTAVYYCARVGPVSWDDSPQDNYMDVWGKGTIV 120
DB 61 FQDRVTFDTATSANTAYMELRLSRASDTAVYYCARVGPVSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 25
AAR75572
ID AAR75572 standard; protein; 124 AA.
XX AAR75572;
XX AC AAR75572;
XX DT 05-MAR-1996 (first entry)
XX DE VH Fab 3b9 binds to gp120.
XX KW Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
XX KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
XX KW immunoreaction; neutralisation; passive immunotherapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
```

FT Region 1. .27
 FT /label= FR1
 FT Region 28. .32
 FT /label= CDR1
 FT Region 33. .46
 FT /label= FR2
 FT Region 47. .63
 FT /label= CDR2
 FT Region 64. .95
 FT /label= FR3
 FT Region 96. .113
 FT /label= CDR3
 FT Region 114. .124
 FT /label= FR4
 XX WO9511317-A1.
 XX
 XX 27-APR-1995.
 XX
 XX 19-OCT-1994; 94WO-US011907.
 XX
 XX 19-OCT-1993; 93US-00139409.
 XX 26-APR-1994; 94US-00233619.
 XX 19-SEP-1994; 94US-00308841.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Barbas CF, Burton DR, Lerner RA;
 XX
 XX WPI; 1995-170235/22.
 XX
 XX Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
 PT induced disease.
 XX
 XX Claim 6; Page 172-173; 249pp; English.
 XX
 XX The sequences given in AAR75568-72 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
 CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
 CC have randomised amino acids in the entire CDR1 and in four of the 18
 CC amino acid residues in CDR3. These Fab's are used in the production of a
 CC human monoclonal antibody (MAB) which is capable of immunoreacting with,
 CC and neutralising HIV. The MAB's are capable of reducing HIV infectivity
 CC titre in an in vitro virus infectivity assay by 50% at a concentration of
 CC <100 ng of antibody per ml. They can be used to provide passive
 CC immunotherapy to HIV in a human. They neutralise HIV more effectively
 CC than antibodies selected from non-randomised combinatorial libraries
 XX
 XX Sequence 124 AA;
 XX
 Query Match 96.9%; Score 653; DB 2; Length 124;
 Best Local Similarity 96.0%; Pred. No. 1.le-58;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFEMWGWINPYNGKFSK 60
 Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFEMWGWINPYNGKFSK 60
 Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPWDDSPQDNYMDVWGKGTIV 120
 Qy 121 IVSS 124
 Db 121 IVSS 124
 RESULT 26
 AAR75570
 ID AAR75570 standard; protein; 124 AA.
 XX
 AC AAR75570;

XX 05-MAR-1996 (first entry)
 XX
 XX VH Fab 3b3 binds to gp120.
 XX
 XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1, 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAb;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Region 1. .27
 FT /label= FR1
 FT Region 28. .32
 FT /label= CDR1
 FT Region 33. .46
 FT /label= FR2
 FT Region 47. .63
 FT /label= CDR2
 FT Region 64. .95
 FT /label= FR3
 FT Region 96. .113
 FT /label= CDR3
 FT Region 114. .124
 FT /label= FR4
 XX
 XX WO9511317-A1.
 XX
 XX 27-APR-1995.
 XX
 XX 19-OCT-1994; 94WO-US011907.
 XX
 XX 19-OCT-1993; 93US-00139409.
 XX 26-APR-1994; 94US-00233619.
 XX 19-SEP-1994; 94US-00308841.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Barbas CF, Burton DR, Lerner RA;
 XX
 XX WPI; 1995-170235/22.
 XX
 XX Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
 PT induced disease.
 XX
 XX Claim 6; Page 171; 249pp; English.
 XX
 XX The sequences given in AAR75568-72 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
 CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
 CC have randomised amino acids in the entire CDR1 and in four of the 18
 CC amino acid residues in CDR3. These Fab's are used in the production of a
 CC human monoclonal antibody (MAB) which is capable of immunoreacting with,
 CC and neutralising HIV. The MAB's are capable of reducing HIV infectivity
 CC titre in an in vitro virus infectivity assay by 50% at a concentration of
 CC <100 ng of antibody per ml. They can be used to provide passive
 CC immunotherapy to HIV in a human. They neutralise HIV more effectively
 CC than antibodies selected from non-randomised combinatorial libraries
 XX
 XX Sequence 124 AA;
 XX
 Query Match 96.7%; Score 652; DB 2; Length 124;
 Best Local Similarity 96.0%; Pred. No. 1.4e-58;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFEMWGWINPYNGKFSK 60
 Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFEMWGWINPYNGKFSK 60
 Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

Db	61	QDQRTVFTADTTSANTAYMELSLRSADTAVYVCARVGEWGDSDSPQNYMDVWGKGTIV	120
Qy	121	IVSS 124	
Db	121	IVSS 124	
RESULT 27			
AA44346			
ID	AA44346	standard; protein; 250 AA.	
XX	AC		
XX	AA44346;		
DT	14-MAR-2000	(first entry)	
XX	3B3 antibody.		
XX	3B3 antibody; immunotoxin; variable fragment; Fv; gp120 coat protein; exotoxin; PE38; Human immunodeficiency virus type 1; HIV-1; specificity; combinatorial phage display library; bone marrow RNA; connector peptide; cytotoxic moiety; transformed cell line; transplant; quantify.		
KW	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	129..143	
FT	/label= Linker peptide		
FT	/note= "Links VH and VL regions of 3B3 antibody."		
XX	WO9964073-A2.		
PN			
XX	16-DEC-1999.		
PD			
XX	08-JUN-1999; 99WO-US012909.		
PF			
XX	11-JUN-1998; 98US-0088860P.		
PR			
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
XX	Pastan IH, Bera TK, Kennedy PE, Berger EA, Barbas CF;		
PI			
XX	WPI; 2000-105833/09.		
DR	N-PSDB; AA229448.		
DR			
XX			
PT	Novel recombinant immunotoxin directed against the HIV- 1 gp120 coat protein useful for treating HIV-1 infections.		
PT			
XX	Claim 17; Page 47; 50pp; English.		
PS			
XX			
CC	The present amino acid sequence is the variable fragment (Fv) of 3B3 antibody, isolated from a combinatorial phage display library constructed from bone marrow RNA of an infected individual. It is used in a novel chimeric immunotoxin, that comprises an anti-gp120 antibody, having binding specificity to 3B3(Fv) antibody, that is attached by a connector peptide to a cytotoxic moiety, PE38 derived from P.aeruginosa. The chimeric immunotoxin is used in the treatment of HIV-1 infections. It is capable of specifically targeting and killing cells displaying HIV-1 gp120 coat protein. They can be used ex vivo to reduce and/or eliminate the HIV viral load in the infected cells. It can also be used in establishing transformed cell lines derived from HIV-infected sources. The immunotoxins can also be used for detecting the presence or absence and for quantifying the infected cells		
XX			
XX	Sequence 250 AA;		
Query Match 96.7%; Score 652; DB 3; Length 250;			
Best Local Similarity 96.0%; Pred. No. 3,1e-58;			
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;			
QY	1	LQSGAEVKKPGASVKVSQASGYRFSNFTVHWYRQAPGQRFEMWGWINPYNGKFFSAK	60
Db	5	LQSGAEVKKPGASVKVSQASGYRFSNFTVHWYRQAPGQRFEMWGWINPYNGKFFSAK	64

Qy	61	FQDRVTFADTSANTAYMELSLASDADVYCARVGPYSWDDSPQDNYYMDVMGKGTIV
Dd	65	FQDRVTFADTSANTAYMELSLASDADVYCARVGEWGWDSDPQDNYYMDVMGKGTIV
Qy	121	IYSS 124
Dd	125	IYSS 128
RESULT 28		
AAR54335		
ID	AAR54335	standard; protein; 124 AA.
XX	AC	AAR54335;
DT	25-MAR-2003	(revised)
DT	10-NOV-1994	(first entry)
XX	XX	Anti-HIV gp120 immunoglobulin L12-HC12 shuffled heavy chain.
XX	XX	Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW	KW	neutralisation; monoclonal antibody; heavy chain; shuffled;
KW	KW	variable region; framework; complementarity determining region.
XX	XX	Homo sapiens.
OS	XX	
XX	XX	
PH	XX	Location/Qualifiers
FT	Region	1..31
FT	/label= FR1	
FT	Region	32..36
FT	/label= CDR1	
FT	Region	37..50
FT	/label= FR2	
FT	Region	51..67
FT	/label= CDR2	
FT	Region	68..99
FT	/label= FR3	
FT	Region	100..117
FT	/label= CDR3	
FT	Region	118..124
FT	/label= FR4	
XX	XX	
PN	WO9407922-A1.	
XX	XX	
PD	14-APR-1994.	
XX	XX	
PF	30-SEP-1993;	93WO-US009328.
XX	XX	
PR	30-SEP-1992;	92US-00954148.
XX	XX	
PA	(SCRI)	SCRIPPS RES INST.
XX	XX	
PI	Burton DR,	Barbas CF, Lerner RA;
XX	XX	
DR	WPI;	1994-135516/16.
XX	XX	
PT	New human monoclonal antibodies neutralising HIV - react with gp120 or	
PT	gp41 and nucleic acid encoding them, useful for in vivo or in vitro	
PT	diagnosis and for passive immuno-therapy.	
XX	XX	
PS	Example;	Page 206-207; 248pp; English.
XX	XX	
CC	The anti-HIV gp120 light chain clone b12 (AAR54253) was recombined with a	
CC	heavy chain library to construct a new library Li2-Hcn. Ten heavy chains	
CC	which recombined with the b12 light chain and bound gp120 by panning were	
CC	chosen for sequence analysis. AAR54335 was one of these heavy chains.	
CC	(Updated on 25-MAR-2003 to correct PN field.)	
XX	XX	
SQ	Sequence 124 AA;	
Query Match	95.8%;	Score 646; DB 2; Length 124;
Best Local Similarity	96.7%;	Pred. No. 5.6e-58;
Matches 116:	Conservative	3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKKEFSAK 60
 DB 5 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKKEFSAK 64
 QY 61 FQDRVTFTADTTSANTAYMELSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 65 FRDRVTFTADTDANTAYMELSLRSADTAIVYCARVGPYTWDDSPQDNYMDVWGKTTV 124

RESULT 29
 AA001309
 ID AA001309 standard; protein; 124 AA.
 XX AC AA001309;
 XX DT 29-JAN-1997 (first entry)
 XX VH region of HIV neutralising MAb, clone HC12.
 XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 1..31
 FT /label= FR1
 FT Region 32..36
 FT /label= CDR1
 FT Region 37..50
 FT /label= FR2
 FT Region 51..67
 FT /label= CDR2
 FT Region 68..99
 FT /label= FR3
 FT Region 100..117
 FT /label= CDR3
 FT Region 118..124
 FT /label= FR4

XX WO9602273-A1.
 XX PD 01-FEB-1996.
 XX PF 11-JUL-1995; 95WO-US008743.
 XX PR 18-JUL-1994; 94US-00276852.
 XX (SCRI) SCRIPPS RES INST.
 XX FI Burton DR, Barbas CF, Lerner RA;
 XX WPI; 1996-179601/18.
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 FT immunotherapy and detection of HIV infection.
 XX Example; Fig 13; 366pp; English.

XX The sequences given in AA001302-11 represent the heavy chain variable
 CC regions (VH) of a series of monoclonal antibodies (MAb's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the gene
 CC clone, HC12. These sequences represent heavy chains which bind to the b12
 CC light chain clone (see also AA001276). These sequences were isolated from
 CC the shuffled heavy chain library, Hn-Li2. A MAb containing this VH
 CC sequence has the capacity to reduce HIV infectivity titre in an in vivo
 CC virus infectivity assay by 50 % at a concentration of less than 700 ng of
 CC antibody/ml, and binds mature gp120 preferentially over the precursor
 CC gp160. The MAb may be used for determining immunocompetence of a human

CC anti-HIV antibody and in the detection of HIV infection. The heavy chain
 CC clones designated H2 and H14 exhibited approx. 40 % neutralisation of HIV
 CC in a syncytia assay
 XX Sequence 124 AA;
 SQ Query Match 95.8%; Score 646; DB 2; Length 124;
 Best Local Similarity 96.7%; Pred. No. 5.6e-58;
 Matches 116; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKKEFSAK 60
 DB 5 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKKEFSAK 64
 QY 61 FQDRVTFTADTTSANTAYMELSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 65 FRDRVTFTADTDANTAYMELSLRSADTAIVYCARVGPYTWDDSPQDNYMDVWGKTTV 124

RESULT 30
 AA001309
 ID AA001309 standard; protein; 124 AA.
 XX AC AA001309;
 XX DT 04-JUL-2000 (first entry)
 XX Anti-gp120 HC12 heavy chain variable amino acid sequence.
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX OS Homo sapiens.
 XX AU9948754-A.
 XX PD 17-FEB-2000.
 XX PF 16-SEP-1999; 99AU-00048754.
 XX PR 16-SEP-1999; 99AU-00048754.
 XX (SCRI) SCRIPPS RES INST.
 XX FI Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-246867/22.
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 FT (HIV) used for providing passive immunotherapy to HIV are specific for
 FT glycoprotein-120.
 XX Example 9; Fig 13; 374pp; English.

XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AA001302) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease

CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
XX derivation
SQ Sequence 124 AA;

Query Match 95.8%; Score 646; DB 3; Length 124;
Best Local Similarity 96.7%; Pred. No. 5.6e-58;
Matches 116; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFHWGWINPYNGNKEFSAX 60
Db |||||
5 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFHWGWINPYNGNKEFSAX 64
QY 61 FQDRVTFADTANTAYMELRSLSRSDTAIYVCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db |||||
65 FRDRVTFADTANTAYMELRSLSRSDTAIYVCARVGPYTWDDSPQDNYMDVWGKGTIV 124

Search completed: August 26, 2004, 13:37:42
Job time : 49.4667 secs

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:57 ; Search time 38.3926 Seconds
(without alignments)
1199.858 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MEWSWVLEFLSVTCVHSQ.....PODNYMDVWGKTTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL-25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497	62.7	614	Q96GA6	Q96GA6 homo sapien
2	483.5	51.0	500	Q9BRV0	Q9BRV0 homo sapien
3	471.5	59.5	159	Q96QSO	Q96QSO homo sapien
4	468.5	59.1	613	Q8VCX7	Q8VCX7 mus musculus
5	468	59.0	168	Q8VDC9	Q8VDC9 mus musculus
6	453.5	57.2	473	Q91L25	Q91L25 mus musculus
7	448.5	56.6	469	Q7Z7P5	Q7Z7P5 homo sapien
8	445	56.1	437	Q8WY24	Q8WY24 homo sapien
9	441	55.6	489	Q8VCX4	Q8VCX4 mus musculus
10	440	55.5	470	Q7TMK1	Q7TMK1 mus musculus
11	440	55.5	473	Q9D8L4	Q9D8L4 mus musculus
12	428	54.0	481	Q91WT1	Q91WT1 mus musculus
13	425	53.6	150	Q9Y298	Q9Y298 homo sapien
14	423	53.3	468	Q91L31	Q91L31 mus musculus
15	416.5	52.5	481	Q8VCV5	Q8VCV5 mus musculus
16	412.5	52.0	463	Q99LC4	Q99LC4 mus musculus

17	412	52.0	119	5	Q9GYZ2	Q9GYZ2 schistosoma
18	412	52.0	480	11	Q8K0Z4	Q8K0Z4 mus musculus
19	411.5	51.9	278	11	Q921K1	Q921K1 mus musculus
20	407.5	51.4	482	11	Q8K172	Q8K172 mus musculus
21	407.5	51.4	498	11	Q8K0F2	Q8K0F2 mus musculus
22	407	51.3	119	4	Q9UL94	Q9UL94 homo sapien
23	406.5	51.3	124	4	Q9UL92	Q9UL92 homo sapien
24	405.5	51.1	488	11	Q91WR1	Q91WR1 mus musculus
25	404	50.9	125	4	Q9UL95	Q9UL95 homo sapien
26	400	50.4	614	11	Q7TWT6	Q7TWT6 mus musculus
27	398.5	50.3	496	4	Q96DK0	Q96DK0 homo sapien
28	398	50.2	157	4	Q95978	Q95978 homo sapien
29	398	50.2	474	11	Q8R3H6	Q8R3H6 mus musculus
30	395	49.8	484	11	Q99LA6	Q99LA6 mus musculus
31	382.5	48.2	116	4	Q9UL89	Q9UL89 homo sapien
32	371	46.8	481	11	Q91WT3	Q91WT3 mus musculus
33	364.5	46.0	145	11	Q924R3	Q924R3 mus musculus
34	364	45.9	142	11	Q924Q1	Q924Q1 mus musculus
35	362.5	45.7	143	11	Q924R0	Q924R0 mus musculus
36	362	45.6	144	11	Q924P5	Q924P5 mus musculus
37	358.5	45.2	143	11	Q924Q5	Q924Q5 mus musculus
38	357.5	45.1	145	11	Q924R4	Q924R4 mus musculus
39	355	44.8	146	11	Q924Q3	Q924Q3 mus musculus
40	355	44.8	147	11	Q925S3	Q925S3 mus musculus
41	354.5	44.7	109	11	Q9JL75	Q9JL75 mus musculus
42	354.5	44.7	143	11	Q91V67	Q91V67 mus musculus
43	354	44.6	117	11	Q9QXF0	Q9QXF0 mus musculus
44	353.5	44.6	145	11	Q924Q6	Q924Q6 mus musculus
45	353	44.5	117	11	Q9QXE9	Q9QXE9 mus musculus
46	352.5	44.5	145	11	Q924Q7	Q924Q7 mus musculus
47	352.5	44.5	145	11	Q924R1	Q924R1 mus musculus
48	352	44.4	146	11	Q924R8	Q924R8 mus musculus
49	348.5	43.9	145	11	Q924Q9	Q924Q9 mus musculus
50	348	43.8	140	11	Q924P8	Q924P8 mus musculus
51	347.5	43.8	143	11	Q924R7	Q924R7 mus musculus
52	346.5	43.7	241	11	Q921A6	Q921A6 mus musculus
53	346	43.6	140	11	Q924R2	Q924R2 mus musculus
54	345.5	43.6	141	11	Q924Q4	Q924Q4 mus musculus
55	345.5	43.6	145	11	Q924P7	Q924P7 mus musculus
56	342.5	43.2	143	11	Q91VA2	Q91VA2 mus musculus
57	341.5	43.1	137	11	Q924R6	Q924R6 mus musculus
58	341.5	43.1	143	11	Q924Q0	Q924Q0 mus musculus
59	339.5	42.8	118	11	Q921C4	Q921C4 mus musculus
60	339	42.7	123	11	Q8VJ11	Q8VJ11 mus musculus
61	337.5	42.6	613	4	Q8WUX1	Q8WUX1 homo sapien
62	335.5	42.3	143	11	Q924P9	Q924P9 mus musculus
63	335.5	42.3	573	4	Q8WU38	Q8WU38 homo sapien
64	335	42.2	146	11	Q924Q8	Q924Q8 mus musculus
65	335	42.2	170	11	Q925S2	Q925S2 mus musculus
66	331	41.7	142	11	Q924Q2	Q924Q2 mus musculus
67	329.5	41.6	243	11	Q7TGM2	Q7TGM2 mus musculus
68	328	41.4	111	11	Q9D9B8	Q9D9B8 mus musculus
69	328	41.4	479	11	Q91WP5	Q91WP5 mus musculus
70	327	41.2	499	4	Q8N5K4	Q8N5K4 homo sapien
71	326.5	41.2	143	11	Q924P6	Q924P6 mus musculus
72	326	41.1	120	11	Q920E8	Q920E8 mus musculus
73	324.5	40.9	114	11	Q9JL81	Q9JL81 mus musculus
74	324.5	40.9	139	11	Q924R5	Q924R5 mus musculus
75	320.5	40.4	110	11	Q9JL77	Q9JL77 mus musculus
76	318.5	40.2	136	11	Q7TPE3	Q7TPE3 mus musculus
77	317	40.0	484	11	Q8VEA0	Q8VEA0 mus musculus
78	315	39.7	121	11	Q8CGS2	Q8CGS2 mus musculus
79	313.5	39.5	218	11	Q925S1	Q925S1 mus musculus
80	313	39.5	493	4	Q8NCL6	Q8NCL6 homo sapien
81	313	39.5	597	4	Q96BB9	Q96BB9 homo sapien
82	310	39.1	109	11	Q9JL85	Q9JL85 mus musculus
83	309	39.0	482	4	Q7Z351	Q7Z351 homo sapien
84	308	38.8	117	11	Q9ZIC6	Q9ZIC6 mus musculus
85	297.5	37.5	110	11	Q9JL83	Q9JL83 mus musculus
86	295.5	37.3	473	11	Q91Z05	Q91Z05 mus musculus
87	295	37.2	113	4	Q9UL90	Q9UL90 homo sapien
88	294.5	37.1	487	11	Q99KX4	Q99KX4 mus musculus
89	294	37.1	521	4	Q8N4Y9	Q8N4Y9 homo sapien

90 293 36.9 588 4 Q8WDX4
 Q96GA6 91 293 36.9 597 4 Q9BUL0
 AC Q96GA6; 92 293 36.9 618 4 Q96AA6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created) 93 292 36.8 469 11 Q8R3V9
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 94 290.5 36.6 298 11 Q9QYF0
 DE Hypothetical protein. 95 290 36.6 487 11 Q8Q217
 OS Homo sapiens (Human) 96 289.5 36.5 147 4 Q9V509
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; 97 289 36.4 480 11 Q91XE1
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 98 289 36.4 597 4 Q9B9B8
 NCBI_TaxID=9606; 99 288 36.3 116 4 Q9UL93
 RN 100 284.5 35.9 494 4 Q96K68

ALIGNMENTS

RESULT 1
 Q96GA6 PRELIMINARY; PRT; 614 AA.
 AC Q96GA6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN 1
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009851; AAH09851.1; -
 DR PIR; S15590; S15590
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000005; HTHARAC.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67921 MW; 55EP536E77AA9BBB CRC64;
 Query Match 62.7%; Score 497; DB 4; Length 614;
 Best Local Similarity 63.0%; Pred. No. 5.8e-44;
 Matches 92; Conservative 17; Mismatches 31; Indels 6; Gaps 1;
 QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQVGRFSNFIHWVRQAP 60
 DB 1 MDWTWRLFLVAATDAYSQVQLVQSGAEVKK:GSSVKVSKASGTFYRILHWVRQAP 60
 QY 61 GQFPEWGWNPYNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYICARVGF 120
 DB 61 GQALEWGWITPENGNTNYAQKQDRVTITRDSMNTAYMELSLRSADTAVYICARGYS 120
 QY 121 YSWDDSPQDNYNDVGVKGTITVSS 146
 DB 121 SSWDDA-----FDIQCQGNITVSS 140

RESULT 2
 Q9BRV0 PRELIMINARY; PRT; 500 AA.
 AC Q9BRV0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN 1
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005951; AAH05951.1; -
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43P2A3CC6D9 CRC64;
 Query Match 61.0%; Score 483.5; DB 4; Length 500;
 Best Local Similarity 63.9%; Pred. No. 1.2e-42;
 Matches 94; Conservative 12; Mismatches 40; Indels 1; Gaps 1;
 QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQVGRFSNFIHWVRQAP 60
 DB 1 MDWTWRLFLVAATGAQSQVHLVQSGAEVMSFGASVRSCKTSGYAFHYISIIWVRQAP 60
 QY 61 GQFPEWGWNPYNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYICARV 119
 DB 61 GQGLEWGWISPSDNTFRFAKKFQGRVTLTTDTSTVYMELSLRSDDTAVYICARRYC 120
 QY 120 YSWDDSPQDNYNDVGVKGTITVSS 146
 DB 121 SYSSCONDYIIYNDVGVKGTITVSS 147
 RESULT 3
 Q96QSO PRELIMINARY; PRT; 159 AA.
 ID Q96QSO
 AC Q96QSO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative matrix cell adhesion molecule-3.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN 1
 RP SEQUENCE FROM N.A.
 RA Tilson M.D.;
 RT mRNA
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY039025; AAK82649.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;
 Query Match 59.5%; Score 471.5; DB 4; Length 159;
 Best Local Similarity 61.7%; Pred. No. 5.5e-42;
 Matches 92; Conservative 18; Mismatches 36; Indels 3; Gaps 1;
 QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQVGRFSNFIHWVRQAP 60
 DB 1 MDWTWRLFLVAATGAQSQVHLVQSGAEVMSFGASVRSCKTSGYAFHYISIIWVRQAP 60


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QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQCSQASGYRFSNFIHWVRQAP 60
Db 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQCSQASGYRFSNFIHWVRQAP 60
QY 61 GORFEMWGNIPYNGKPEKAFQDRVTFTADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GQGLEWIGLWNPNGSGSIKFKNEKFKATLTADKSSITVYMDLSRLSLSADTAVVYCARVGP 117
QY 121 YSWDDSPQDNY-----YMDVWVGKGTIVVSS 146
Db 118 ---HEDRGNYDGLAWFVWVGQGTIVTVA 144

RESULT 10
Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=2238822; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 2
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH55910.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 55.5%; Score 440; DB 11; Length 470;
Best Local Similarity 57.5%; Pred. No. 4.6e-38;
Matches 84; Conservative 22; Mismatches 34; Indels 6; Gaps 2;

QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQCSQASGYRFSNFIHWVRQAP 60
Db 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQCSQASGYRFSNFIHWVRQAP 60
QY 61 GORFEMWGNIPYNGKPEKAFQDRVTFTADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GQGLEWIGLWNPNGSGSIKFKNEKFKATLTADKSSITVYMDLSRLSLSADTAVVYCARVGP 117
QY 121 YSWDDSPQDNY-----YMDVWVGKGTIVVSS 146
Db 118 YVYSGS---YVYFDVWVGAGTIVTVA 140

RESULT 12
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1
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RESULT 11
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4;
AC Q9D8L4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE 1810060009rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido I., Furuno M., Aono H., Baidarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka O., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
DR PIR; S26746; S26746.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 55.5%; Score 440; DB 11; Length 473;
Best Local Similarity 57.5%; Pred. No. 4.7e-38;
Matches 84; Conservative 24; Mismatches 30; Indels 8; Gaps 2;

QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQCSQASGYRFSNFIHWVRQAP 60
Db 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQCSQASGYRFSNFIHWVRQAP 60
QY 61 GORFEMWGNIPYNGKPEKAFQDRVTFTADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GQGLEWIGLWNPNGSGSIKFKNEKFKATLTADKSSITVYMDLSRLSLSADTAVVYCARVGP 119
QY 121 YSWDDSPQDNY-----YMDVWVGKGTIVVSS 146
Db 120 YDYD-----WFAYWVGQGTIVTVA 138

RESULT 12
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1
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RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029188; AAH29188.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG1; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 2.
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 52.0%; Score 412; DB 11; Length 480;
Best Local Similarity 52.7%; Pred. No. 4.4e-35;
Matches 78; Conservative 26; Mismatches 30; Indels 14; Gaps 2;

Qy 1 MENSWVLFLLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGRWIFLFLSGTAGVHCQVQLQSGPELVKFGALVKISKASGYTFTSFDISNKKRP 60

Qy 61 GQRFEMGWINPYNGKFEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCAR--V 118
Db 61 GQGFEMGWISPGDGSSEYNEKFKGKATLTADKSSNTAYMHLSSLTSSENSAVYFCARSKL 120.

Qy 119 GPYSWDDSPQDNYMDVWGKTTIVSS 146
Db 121 GGFAY-----WGQGLTVTVSA 136

RESULT 19
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 51.9%; Score 411.5; DB 11; Length 278;
Best Local Similarity 53.4%; Pred. No. 2.5e-35;
Matches 78; Conservative 24; Mismatches 37; Indels 7; Gaps 2;

Qy 1 MENSWVLFLLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGNWCIILFLVATATGVHSQVQLQPGAEVLKPGASVKLSCKASGYTFTSYNHWVQR 60

Qy 61 GQRFEMGWINPYNGKFEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGP 120
Db 61 GQGLEWICINPNSSGGTNYNEKFKGKATLAVDKSSSTVYMQLSLTSSEDSAVYYCTR--G 118

Qy 121 YSWDDSPQDNYMDVWGKTTIVSS 146

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Db 119 YGYDD-----VYFDVWGAGTTTVSS 139

RESULT 20
Q8K172 PRELIMINARY; PRT; 482 AA.
ID Q8K172;
AC Q8K172;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to expressed sequence AI893595.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028249; AAH28249.1; -.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 2.
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match 51.4%; Score 407.5; DB 11; Length 482;
Best Local Similarity 52.1%; Pred. No. 1.3e-34;
Matches 76; Conservative 25; Mismatches 36; Indels 9; Gaps 1;

Qy 1 MENSWVLFLLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGNWCIILFLAATATGVHSQVQLQPGAEVLKPGASVKLSCKASGYTFTSYNHWVQR 60

Qy 61 GQRFEMGWINPYNGKFEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGP 120
Db 61 GRGLEWIGRIDPNSSGGTNYNEKFKGKATLTVDKPSSTAYMQLSLTSSEDSAVYYCTREGD 120

Qy 121 YSWDDSPQDNYMDVWGKTTIVSS 146
Db 121 YD-----AMDYWGQTSVTVSS 137

RESULT 21
Q8K0F2 PRELIMINARY; PRT; 488 AA.
ID Q8K0F2;
AC Q8K0F2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to expressed sequence A1893585.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.
 RE EMBL; BC031703; AAH31703.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00407; IG1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_YHC; 2.
 SQ SEQUENCE 488 AA; 53127 MW; 0B3B156E1E5733F0 CRC64;

Query Match 51.4%; Score 407.5; DB 11; Length 488;
 Best Local Similarity 52.7%; Pred. No. 1.4e-34;
 Matches 77; Conservative 26; Mismatches 40; Indels 3; Gaps 1;

QY 1 MEWSWVFLFSLVTGTVHSQVOLVOSGAEVKKPGASVKVSCQASGYRFSNFIHWVQAP 60
 DB 1 MGWSCIMFLFAAATGTVHSQVOLQOPGTGLVKPGASVKLSCKASGYTFTSYWVHWVKQP 60
 QY 61 GQREPWGWINPYNGNKFEKAFQDRVTFTADTSANTAYMELRLSRGADTAVVYCARVGP 120
 DB 61 GRGLEW-GRIDPNSGDIKFEKFKTKATLTVDKPSIVYVHRLSLTSDSAVYVCTRGL 120

QY 121 YSWDDSPQDNYMDVWCKGTIVVSS 146
 DB 121 FY---SDYVDYSMDYWGQGTSTVTVSS 143

RESULT 22
 Q9UL94 PRELIMINARY; PRT; 119 AA.
 ID Q9UL94
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035020; AAD56256.1; -.
 DR HSPF; P01810; 2FEJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 119
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 51.3%; Score 407; DB 4; Length 119;

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GN IGH-VJ558 OR AI933585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL EMBL; EC013539; AAH13539.1; -.
DR SUBMITTED (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR MGI; 96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match
Best Local Similarity 50.3%; Score 405.5; DB 11; Length 488;
Matches 76; Conservative 30; Mismatches 32; Indels 13; Gaps 3;

QY 1 MEWSWFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWNWFLFLSVTTAGIYSEVQLQSGPELVKPGASVKLSCKASGYTIDYYNWKQSH 60

QY 61 GQFEWGWINPYNKKEFSAKFDQRTVFTADTSANTAYMELSLRSADTAVYCARVGP 120
DB 61 GKSLEWIGDINPYNKGSYNGKFKGKATLTVDKSSSIAYMQLNNLTSDSASVYCAR-GP 119

QY 121 ----YSWDDSPQDNYMDVWGKTTIVSS 146
DB 120 VYISYFSYDRG-----DIWGQTLVTVSA 143

RESULT 25
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSPB; AF035019; AAD56255.1; -.
DR HSPB; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 125
SQ SEQUENCE 125 AA; 13516 MW; OD3CD5C232488EAC CRC64;

Query Match
Best Local Similarity 50.9%; Score 404; DB 4; Length 125;
Matches 76; Conservative 30; Mismatches 32; Indels 13; Gaps 3;

QY 1 MEWSWFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWNWFLFLSVTTAGIYSEVQLQSGPELVKPGASVKLSCKASGYTIDYYNWKQSH 60

QY 61 GQFEWGWINPYNKKEFSAKFDQRTVFTADTSANTAYMELSLRSADTAVYCARVGP 120
DB 61 GKSLEWIGDINPYNKGSYNGKFKGKATLTVDKSSSIAYMQLNNLTSDSASVYCAR-GP 119

QY 121 ----YSWDDSPQDNYMDVWGKTTIVSS 146
DB 120 VYISYFSYDRG-----DIWGQTLVTVSA 143

RESULT 26
Q7TMT6 PRELIMINARY; PRT; 614 AA.
AC Q7TMT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; EC033409; AAH53409.1; -.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF38BD124F89 CRC64;

Query Match
Best Local Similarity 50.4%; Score 400; DB 11; Length 614;
Matches 78; Conservative 25; Mismatches 35; Indels 8; Gaps 2;

QY 1 MEWSWFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MEWPFILFLSVTTGVHSQVQLQSGPELVKPGASVKISKASGYAFSSWMVWKQRP 60

QY 61 GQFEWGWINPYNKKEFSAKFDQRTVFTADTSANTAYMELSLRSADTAVYCARVGP 120
DB 61 GKLEWIGRVYVPGDITNYNGKFKGKATLTADKSSSIAYMQLNNLTSDSASVYCAR--D 118

QY 121 YSWDDSPQDNYMDVWGKTTIVSS 146

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Db 119 YG-----SSRYFAYGQGLTVTSA 138
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RESULT 27
Q96DK0 PRELIMINARY; PRT; 496 AA.
AC Q96DK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ35299.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastric mucosa;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiracka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058027; BAB71633.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53532 MW; C72BE1E247C86FED CRC64;

Query Match 50.3%; Score 398.5; DB 4; Length 496;
Best Local Similarity 54.8%; Pred. No. 1.2e-33;
Matches 80; Conservative 15; Mismatches 48; Indels 3; Gaps 1;

QY 1 MEWSVFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
|||:|||||
Db 1 MDWTRFLFVAATGVQSQVHLVQSGAEIKKPGASVKVKCKSANFSAFTWVRQAP 60
|||:|||||
QY 61 GQFPEWGWINPNYNGKFSQAKFQDRVTFTADTSANTAYMELRSLSADTAVYICARVGP 120
|||:|||||
Db 61 GQGLQWGGIIPNFGAPVNAQFQDRVTISADDSITTVYMLTSLFTFATFYCGRGLT 120
|||:|||||
QY 121 YSWDDSPQDNYVMDVWGKGTIVVSS 146
|||:|||||
Db 121 YGSGS---YYLQHWGQGLTVVSS 143
|||:|||||

RESULT 28
Q95978 PRELIMINARY; PRT; 157 AA.
AC Q95978;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vhl protein precursor (Fragment).
GN VHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PerIPHERAL blood;
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
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RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularity Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ005570; CAA06599.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 869865EDDA84D88B5 CRC64;

Query Match 50.2%; Score 398; DB 4; Length 157;
Best Local Similarity 54.8%; Pred. No. 3.4e-34;
Matches 80; Conservative 16; Mismatches 44; Indels 6; Gaps 2;

QY 1 MEWSVFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
|||:|||||
Db 1 MDWTRFLFVAATGVQSQVHLVQSGAEIKKPGASVKVKCKSGYVFTSYIIHWVRQPR 60
|||:|||||
QY 61 GQFPEWGWINPNYNGKFSQAKFQDRVTFTADTSANTAYMELRSLSADTAVYICARVGP 120
|||:|||||
Db 61 GQGLQWGGIIPNFGAPVNAQFQDRVTISADDSITTVYMLTSLFTFATFYCGRGLT 120
|||:|||||
QY 121 YSWDDSPQDNYVMDVWGKGTIVVSS 146
|||:|||||
Db 120 -RM---RSGNYNGHWGQGLTVVSS 140
|||:|||||

RESULT 29
Q9R3H6 PRELIMINARY; PRT; 474 AA.
AC Q9R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 50.2%; Score 398; DB 11; Length 474;
Best Local Similarity 54.1%; Pred. No. 1.3e-33;
Matches 79; Conservative 24; Mismatches 35; Indels 8; Gaps 2;

QY 1 MEWSVFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
|||:|||||
```

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Db      1  MNPWCILLFLLSVTGVSQVQLQSGPELVKPGASVKISCRASGVAFSFSNWNYVTRP 60
QY      61  GQRFWMGWINPYNGKFEFAKFDQRTVTHADTSANTAYNELSLRSADTAVTYCARVP 120
Db      61  GGLGLEWIGRIFFGDDGTHYSFGFGKAKLTADKSSVTFQLQTSLTSEDVAVFCAR--- 117
QY      121  YGWDSDSPQDNYMDVMVGKGTTVVSS 146
Db      118  ----DSDYGDYF-DDMGQGATVVS 138

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RESULT 30

Q99L56	Q99LA6	PRELIMINARY;	PRT;	434 AA.
ID	Q99LA6			
AC	Q99LA6;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.			
EMBL	EMBL; BC003495; AAH03495.1; -.			
DR	PIR; F33932; F33932.			
DR	HSSP; P01610; 2FEJ			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF000047; Ig: 4.			
DR	SMART; SM00406; IGV: 1.			
DR	PROSITE; PS00835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; 2.			
DR	Hypothetical protein.			
KW	SEQUENCE 484 AA; 52567 MW; 8EAFA4F9BCF582FA CRC64;			
SQ				

Search completed: August 26, 2004, 13:39:24
Job time : 39.3926 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:27 Search time 8.65185 Seconds
(without alignments)
878.684 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MEWSWFLFLSVTTGVHSQ.....PQDNYMDVWGKTTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: SwissProt 42.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459.5	57.9	147	1	HVIC_HUMAN
2	433	54.6	117	1	HVIC_HUMAN
3	431	54.4	117	1	HVIC_HUMAN
4	423	53.3	140	1	HVIC_MOUSE
5	408.5	51.5	139	1	HVIC_MOUSE
6	402	50.7	117	1	HVIC_MOUSE
7	391.5	49.4	137	1	HVIC_MOUSE
8	389	49.1	138	1	HVIC_MOUSE
9	383	48.3	117	1	HVIC_MOUSE
10	378.5	47.7	120	1	HVIC_HUMAN
11	375	47.3	117	1	HVIC_MOUSE
12	374	47.2	136	1	HVIC_MOUSE
13	370	46.7	117	1	HVIC_MOUSE
14	362	45.6	120	1	HVIC_MOUSE
15	360	45.4	117	1	HVIC_MOUSE
16	360	45.4	117	1	HVIC_MOUSE
17	357.5	45.1	120	1	HVIC_MOUSE
18	355	44.8	117	1	HVIC_MOUSE
19	354	44.6	117	1	HVIC_MOUSE
20	352	44.4	117	1	HVIC_MOUSE
21	351.5	44.3	118	1	HVIC_MOUSE
22	347	43.8	117	1	HVIC_MOUSE
23	341	43.0	117	1	HVIC_HUMAN
24	339	42.7	125	1	HVIC_HUMAN
25	328.5	41.4	114	1	HVIC_MOUSE
26	321	40.5	121	1	HVIC_MOUSE
27	316.5	39.3	136	1	HVIC_MOUSE
28	311.5	39.3	119	1	HVIC_MOUSE
29	302.5	38.1	144	1	HVIC_MOUSE
30	298.5	37.6	124	1	HVIC_HUMAN
31	296.5	37.4	122	1	HVIC_HUMAN
32	293	36.9	146	1	HVIC_HUMAN
33	292	36.8	119	1	HVIC_HUMAN

34	291	36.7	121	1	HVIC_HUMAN
35	290.5	36.6	122	1	HVIC_HUMAN
36	290.5	36.6	124	1	HVIC_HUMAN
37	289.5	36.5	122	1	HVIC_MOUSE
38	289	36.4	123	1	HVIC_MOUSE
39	288	36.3	123	1	HVIC_MOUSE
40	286.5	36.1	122	1	HVIC_MOUSE
41	285	35.9	123	1	HVIC_MOUSE
42	284	35.8	123	1	HVIC_MOUSE
43	283	35.7	118	1	HVIC_MOUSE
44	283	35.7	123	1	HVIC_MOUSE
45	283	35.7	123	1	HVIC_MOUSE
46	282.5	35.6	119	1	HVIC_MOUSE
47	282	35.6	137	1	HVIC_MOUSE
48	281	35.4	117	1	HVIC_HUMAN
49	279.5	35.2	119	1	HVIC_MOUSE
50	277.5	35.0	119	1	HVIC_HUMAN
51	276	34.8	117	1	HVIC_MOUSE
52	275.5	34.7	126	1	HVIC_MOUSE
53	275	34.7	115	1	HVIC_HUMAN
54	273.5	34.5	122	1	HVIC_HUMAN
55	272	34.3	117	1	HVIC_MOUSE
56	271.5	34.2	116	1	HVIC_MOUSE
57	270.5	34.1	117	1	HVIC_CARAU
58	270	34.0	142	1	HVIC_BAT
59	266.5	33.6	117	1	HVIC_MOUSE
60	265	33.4	144	1	HVIC_MOUSE
61	262	33.0	116	1	HVIC_CARAU
62	261	32.9	119	1	HVIC_HUMAN
63	260.5	32.8	116	1	HVIC_HUMAN
64	259.5	32.7	120	1	HVIC_HUMAN
65	259	32.7	120	1	HVIC_MOUSE
66	258	32.5	117	1	HVIC_MOUSE
67	256.5	32.3	114	1	HVIC_HUMAN
68	255.5	32.2	115	1	HVIC_HUMAN
69	255	32.2	115	1	HVIC_HUMAN
70	254.5	32.1	118	1	HVIC_HUMAN
71	254	32.0	116	1	HVIC_HUMAN
72	253.5	32.0	117	1	HVIC_HUMAN
73	253	31.9	117	1	HVIC_CARAU
74	251.5	31.7	119	1	HVIC_HUMAN
75	250	31.5	116	1	HVIC_MOUSE
76	249.5	31.5	117	1	HVIC_CARAU
77	248	31.3	116	1	HVIC_HUMAN
78	247.5	31.2	114	1	HVIC_CARAU
79	247.5	31.2	119	1	HVIC_HUMAN
80	247	31.1	117	1	HVIC_HUMAN
81	244	30.8	116	1	HVIC_MOUSE
82	244	30.8	117	1	HVIC_MOUSE
83	244	30.8	117	1	HVIC_MOUSE
84	242	30.5	117	1	HVIC_MOUSE
85	242	30.5	117	1	HVIC_MOUSE
86	240	30.3	98	1	HVIC_MOUSE
87	240	30.3	129	1	HVIC_HUMAN
88	239	30.1	135	1	HVIC_XENLA
89	237.5	29.9	111	1	HVIC_MOUSE
90	236.5	29.8	97	1	HVIC_MOUSE
91	235	29.6	117	1	HVIC_CARAU
92	233.5	29.4	116	1	HVIC_MOUSE
93	229	28.9	113	1	HVIC_MOUSE
94	229	28.9	115	1	HVIC_MOUSE
95	225	28.4	115	1	HVIC_MOUSE
96	224.5	28.3	117	1	HVIC_MOUSE
97	224	28.2	113	1	HVIC_MOUSE
98	223.5	28.2	117	1	HVIC_CARAU
99	223	28.1	113	1	HVIC_MOUSE
100	222	28.0	113	1	HVIC_MOUSE

ALIGNMENTS

```

HV1C_HUMAN          STANDARD;          PRT;          147 AA.
ID   HV1C_HUMAN
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DI   16-OCT-2001 (Rel. 40, Last sequence update)
DI   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo I.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVH035.
DR   HSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1..19
FT   CHAIN           20..117   IG HEAVY CHAIN V-I REGION V35.
FT   DOMAIN          20..117   IG-LIKE.
FT   NON_TER         117
FT   SEQUENCE        117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
SQ
Query Match          54.6%; Score 433; DB 1; Length 117;
Best Local Similarity 68.4%; Pred. No. 2.1e-37;
Matches 80; Conservative 12; Mismatches 25; Indels 0; Gaps 0;
QY   1 MEWSVFLFFLSVTTGVHVSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db   1 MDWTWRIFLVAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYTHWVRQAP 60
QY   61 GQFEWGWNPYNGNKEFSAKFDQRTFTADTSANTAYMELSLRSADTAVVYCAR 117
Db   61 GQGLEWGWNPNGSGGTYNAQKFGQRTVTRDTSITAYMELSLRSDDTVVYCAR 117

RESULT 3
HV1B_HUMAN          STANDARD;          PRT;          117 AA.
ID   HV1B_HUMAN
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
DI   21-JUL-1986 (Rel. 01, Last sequence update)
DI   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region HG3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=63144028; PubMed=6298778;
RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RT   (VH) gene subgroups";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
QY   1 MEWSVFLFFLSVTTGVHVSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db   1 MDWTWRIFLVAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYTHWVRQAP 60
QY   61 GQFEWGWNPYNGNKEFSAKFDQRTFTADTSANTAYMELSLRSADTAVVYCAR 117
Db   61 GQGLEWGWNPNGSGGTYNAQKFGQRTVTRDTSITAYMELSLRSDDTVVYCAR 117

HV1C_HUMAN          STANDARD;          PRT;          147 AA.
ID   HV1C_HUMAN
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DI   16-OCT-2001 (Rel. 40, Last sequence update)
DI   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
CC   [2]
CC   SEQUENCE OF 20-147.
RA   Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC   PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   HSP; P01789; IMCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL          1..19
FT   CHAIN           20..147   IG HEAVY CHAIN V-I REGION ND.
FT   DOMAIN          20..131   IG-LIKE.
FT   MOD_RES         20..20
FT   PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID        41..115
FT   CONFLICT        21..21
FT   CONFLICT        53..54   IH -> HI (IN REF. 2).
FT   CONFLICT        67..68   VG -> GV (IN REF. 2).
FT   CONFLICT        125..125 MISSING (IN REF. 2).
FT   NON_TER         147
FT   SEQUENCE        147 AA; 16491 MW; 948F9F72A5366C20 CRC64;
SQ
Query Match          57.9%; Score 459.5; DB 1; Length 147;
Best Local Similarity 59.1%; Pred. No. 5.2e-40;
Matches 86; Conservative 24; Mismatches 35; Indels 3; Gaps 2;
QY   1 MEWSVFLFFLSVTTGVHVSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db   1 MDWTXXXXFLVAATRVHSQTQLVQSGAEVKKPGASVRSCKASGYTFTDSYIHWVRQAP 60
QY   61 GQFEWGWNPYNGNKEFSAKFDQRTFTADTSANTAYMELSLRSADTAVVYCARVGP 120
Db   61 GHGLEWGWNPNGSGGTYNAPRFQGRVTMTDASFTAYMDLRLSLRSDSDSAVFYCAKSDP 120
QY   121 YSND--SPQDNYMDVKGKGTIVSS 146
Db   121 F-WSDYNYFDYSYTLDWGQGTIVTSS 147

RESULT 2
HV1G_HUMAN          STANDARD;          PRT;          117 AA.
ID   HV1G_HUMAN
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DI   01-NOV-1991 (Rel. 20, Last sequence update)
DI   10-OCT-2003 (Rel. 42, Last annotation update)
QY   1 MEWSVFLFFLSVTTGVHVSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db   1 MDWTXXXXFLVAATRVHSQTQLVQSGAEVKKPGASVRSCKASGYTFTDSYIHWVRQAP 60
QY   61 GQFEWGWNPYNGNKEFSAKFDQRTFTADTSANTAYMELSLRSADTAVVYCARVGP 120
Db   61 GHGLEWGWNPNGSGGTYNAPRFQGRVTMTDASFTAYMDLRLSLRSDSDSAVFYCAKSDP 120
QY   121 YSND--SPQDNYMDVKGKGTIVSS 146
Db   121 F-WSDYNYFDYSYTLDWGQGTIVTSS 147

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CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00240; AAAS2988.1; -.
CC PIR; A02024; HVHUNG.
CC HSP; P01772; 2FB4.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC KW IMMUNOGLOBULIN V region; Hydrindoma; Signal.
CC FT SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
CC DOMAIN 20 >117 IG-LIKE.
CC NON TER 117
CC SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 54.4%; Score 431; DB 1; Length 117;
Best Local Similarity 68.4%; Pred. No. 3.3e-37;
Matches 80; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 MEWSVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAP 60
Db 1 MDWTRVFCCLAVAPGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTENSFIHWVROAP 60
QY 61 GQFEWMCWNPYNGKNEKFSKQPDVTFDTADTSANTAYMELRSLSADTAVYYCAR 117
Db 61 GQLEWNGINPESGGSTSAQKPFQGRVTMTTRDTSTSTVMEVSSLSRSEDATVYYCAR 117

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess F., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00493; AAA38128.1; -.

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DR PIR; A94264; HVMSG7.
DR HSP; P01810; 2FBD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hydrindoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 53.3%; Score 423; DB 1; Length 140;
Best Local Similarity 54.8%; Pred. No. 2.7e-36;
Matches 80; Conservative 27; Mismatches 33; Indels 6; Gaps 1;

QY 1 MEWSVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAP 60
Db 1 MGWSFIFLLSVTAGVHSEVQLQSGAEVLRAGSSVKMSCKASGYTFTSYGINVWVQRP 60
QY 61 GQFEWMCWNPYNGKNEKFSKQPDVTFDTADTSANTAYMELRSLSADTAVYYCARVGP 120
Db 61 GQLEWNGINPESGGSTSAQKPFQGRVTMTTRDTSTSTVMEVSSLSRSEDATVYYCARVGP 120
QY 121 YSWDDSPQDNYMDVWVGKGTIVVSS 146
Db 121 YG-----GSYDFYWGQGTPLTVSS 140

RESULT 5
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00529; AAA38170.1; -.
CC PIR; A30809; MHXS18.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.

```

Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 19 IG HEAVY CHAIN V REGION BI-8/186-2.
FT CHAIN 20 139 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 D SEGMENT.
FT DOMAIN 118 124 JH2 SEGMENT.
FT DOMAIN 125 139 BY SIMILARITY.
FT DISULFID 41 115
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 51.58; Score 408.5; DB 1; Length 139;
Best Local Similarity 52.18; Pred. No. 8e-35;
Matches 76; Conservative 26; Mismatches 37; Indels 7; Gaps 1;

Qy 1 MWSWFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGWSIMFLAATATGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Qy 61 GQRFEMGWNPNGNKEFSAKQDQVTFADTSANTAYMELSLRSADTAVYCARVGP 120
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMELSLRSADTAVYCARV 120
Qy 121 YSWDDSPQDNYMDVMGKGTIVVSS 146
Db 121 YG-----SSYFDYWGQGTITLVSS 139

RESULT 6
ID HV14 MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes."
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00488; AAA38519.1; -
CC PIR; A02041; HVMS8A.
CC HSSP; P01810; 2FBJ.
CC MGD; NGL:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
CC DOMAIN 20 117 IG-LIKE.
CC
CC Query Match 49.4%; Score 391.5; DB 1; Length 137;
Best Local Similarity 50.7%; Pred. No. 4.3e-33;
Matches 74; Conservative 24; Mismatches 39; Indels 9; Gaps 1;

FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 50.7%; Score 402; DB 1; Length 117;
Best Local Similarity 60.7%; Pred. No. 3e-34;
Matches 71; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MWSWFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGWSWFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Qy 61 GQRFEMGWNPNGNKEFSAKQDQVTFADTSANTAYMELSLRSADTAVYCAR 117
Db 61 GKSLEWIGIYIPYNGTGKFKSKATLTVDNSSLTAYMELSLTSSEDSAVYCAR 117

RESULT 7
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00539; AAA38172.1; -
CC PIR; A02038; G2MS43.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 122 D SEGMENT.
CC DOMAIN 123 137 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5861BP448BEC9 CRC64;

Query Match 49.4%; Score 391.5; DB 1; Length 137;
Best Local Similarity 50.7%; Pred. No. 4.3e-33;
Matches 74; Conservative 24; Mismatches 39; Indels 9; Gaps 1;

```

QY 1 MEWSWFLFELSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
DB 1 MGWSCIWFLAATATGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
QY 61 GQRFEMWGINPNYNGNKEFSKQDRVTFTADTSANTAYMELRSLSADTAVYICARVGP 120
DB 61 GRGLEWIGRIDPNSGCTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYICARV-- 118
QY 121 YSWDDSPQDNYNDVWGKGTIVVSS 146
DB 119 -----RLGRYFDYWGQGITIVVSS 137

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RESULT 8

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HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HWSM77.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

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Query Match 49.1%; Score 389; DB 1; Length 138;
Best Local Similarity 50.0%; Pred. No. 7.8e-33;
Matches 74; Conservative 25; Mismatches 37; Indels 12; Gaps 2;

```

```

QY 1 MEWSWFLFELSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
DB 1 MGWSCIWFLAATATGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
QY 61 GQRFEMWGINPNYNGNKEFSKQDRVTFTADTSANTAYMELRSLSADTAVYICARVGP 120
DB 61 GQGLEWIGRIDPNSGCTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYICARV--- 117
QY 121 YSWDDSPQDNYNDVWGKGTIVVSS 146
DB 118 -----SDGYDFVFWGQGITIVVSS 138

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RESULT 9

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HV52 MOUSE
ID HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments."
RL Cell 40:271-281(1985).
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CC -----
EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

```

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Query Match 48.3%; Score 383; DB 1; Length 117;
Best Local Similarity 58.1%; Pred. No. 2.7e-32;
Matches 68; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

```

```

QY 1 MEWSWFLFELSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
DB 1 MGWSCIWFLAATATGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
QY 61 GQRFEMWGINPNYNGNKEFSKQDRVTFTADTSANTAYMELRSLSADTAVYICAR 117
DB 61 GQGLEWIGRIDPNSGCTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYICAR 117

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RESULT 10

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HV1H HUMAN
ID HV1H HUMAN STANDARD; PRT; 120 AA.
AC P80421;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclinal
RT immunoglobulins."
RL Eur. J. Biochem. 228:886-893(1995).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP: P01772; 2FB4
DR GO: GO:0005776; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111
FT DISULFID 22 95
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;

Query Match 47.7%; Score 378.5; DB 1; Length 120;
Best Local Similarity 62.7%; Pred. No. 7.9e-32;
Matches 79; Conservative 13; Mismatches 27; Indels 7; Gaps 3;

Qy 21 VOLVQSGAEVKKPGASVKVSCQASGYRFSNFVHVRQAPQGFQFVWGMINPYNGKERS 80
Db 2 VOLVQSGVERKVPQASVRSCKASGVAFENYIHVRQAPGLGLENWGLFNPVAGAVS-S 60

Qy 81 AKFQDRTFTADTSANTAYMELSLRSADTAVYYCARVGVSDSDSPQNYMDVWGKQT 140
Db 61 EKFRDLVMSDTSANTVSMQLNRLSDDTGRYFCARV---SYDFS---QYGMVDVWGQGT 114

Qy 141 TVIVSS 146
Db 115 TVIVSS 120

RESULT 11
HV09 MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P1271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6783376;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR: D90BC9; HVMS61.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT NON TER 117
FT DOMAIN 20 49
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 47.3%; Score 375; DB 1; Length 117;
Best Local Similarity 57.3%; Pred. No. 1.8e-31;
Matches 67; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MEWSWVFLFSLVTGVHVSQVLVQSGAEVKKPGASVKVSCQASGYRFSNFVHVRQAP 60
Db 1 MGWSCIMFLAATATGVHVSQVLQPGAEIVKPGASVKLSCKASGYTFTSYWHVQRQP 60

Qy 61 GQFEWGMWINPYNGKERSAKFQDRTFTADTSANTAYMELSLRSADTAVYYCAR 117
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSTAYMQLSLTSEDSAVYYCAR 117

RESULT 12
HV15 MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00494; AAA38130.1; -.
CC PIR: A02042; HVMSB1.
CC HSP: P01772; 2FB4.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003596; IG_v.
CC Pfam: PF00047; ig; 1.
CC SMART: SM00406; Igv; 1.
CC PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136
FT DOMAIN 20 135
FT NON TER 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 47.2%; Score 374; DB 1; Length 136;
Best Local Similarity 47.9%; Pred. No. 2.6e-31;
Matches 70; Conservative 26; Mismatches 40; Indels 10; Gaps 2;

Qy 1 MEWSWVFLFSLVTGVHVSQVLVQSGAEVKKPGASVKVSCQASGYRFSNFVHVRQAP 60
Db 1 MGWSCIMFLAATATGVHVSQVLQPGAEIVKPGASVKLSCKASGYTFTSYWHVQRQP 60

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Db 1 MGWSCIFFFLVATGATGHSQVQLQSGPEVVRPGVSVKISCKSGYTFDTYAMHWKQSH 60
QY 61 GQFEFWGWINPNYNGKPEAKFQDRVTFADTSANTAYMELSLRSADTAVYICARVGP 120
Db 61 AKSLEWIGVISTYNGTSYNQKFKGATMTVDKSSSTVHMLARLTSEDSANLYCARY-- 118
QY 121 YSWDDSPQDNYMDVWGKGTVTIVSS 146
Db 119 -YGNYP-DYWGQGTTLTVSS 136

RESULT 13
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -! MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -! RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 58
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 46.7%; Score 370; DB 1; Length 117;
Best Local Similarity 57.3%; Pred. No. 5.7e-31;
Matches 67; Conservative 20; Mismatches 30; Indels 0; Gaps 0;

QY 1 MWSWFLFFLSVTGHSQVQLQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGWSCILFLVAANGVHSQVQLQPGTELVKPGASVKLSCKASGYTFYSYHWHVKQRP 60
QY 61 GQFEFWGWINPNYNGKPEAKFQDRVTFADTSANTAYMELSLRSADTAVYICAR 117
Db 61 GQGLEWIGNIPNGGNTNYNEKFSKVTLTVDKSSSTAVYICAR 117

RESULT 14
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
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DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=8131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -! MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111
FT NON_TER 120 120
FT SIGNAL 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 45.6%; Score 362; DB 1; Length 120;
Best Local Similarity 54.0%; Pred. No. 3.9e-30;
Matches 68; Conservative 25; Mismatches 27; Indels 6; Gaps 1;

QY 21 VOLVSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQRFQWGMWINPNYNGKFS 80
Db 1 VOLQSGAEVLRAGSSVXVSKASGYTFYSYHWHVKQRPQGLEWIGNIPNGYTKYN 60
QY 81 AKFQDRVTFADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 140
Db 61 EKFKGKTLTVDKSSSTAYMQLSLTSEDSAVYICARSVYVG-----GSYFYDWGQGT 114
QY 141 TVIVSS 146
Db 115 TLTVSS 120

RESULT 15
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -! MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -! RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02032; HVMS02.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
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FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; 38862FAC67ABD345 CRC64;

Query Match
Best Local Similarity 44.4%; Score 352; DB 1; Length 117;
Matches 63; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 1 MEWSVFLFFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWSCIMFLAATATGVHSPVQLQPGAEVLKPGASVKLSKASGYTFTSYMHWVKQRP 60
QY 61 GORFEWGWINPYNGNKEFSKAFQDRVTFADTSANTAYMELSLRSADTAVYYCAR 117
DB 61 GRGLEWIGNIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSLTSSEDSAVYYCTR 117

RESULT 21
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Sikevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes."
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MMS38.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00835; IG LIKE; 1.
DR KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match
Best Local Similarity 44.3%; Score 351.5; DB 1; Length 118;
Matches 68; Conservative 21; Mismatches 29; Indels 9; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGORFEWGWINPYNGNKEF 79
DB 1 EVQLQSGPELVKPGASVKISCKASGYTFTDYYMHWYKQSHGKSLKLEIGDINPNNGTSS 60
QY 80 SAKFQDRVTFADTSANTAYMELSLRSADTAVYYCARVPSYWDSDSPQDNYMDVWGKG 139
DB 61 NQKFKGATLTVDKSSATYMWELSLRSADTAVYYCAR--GYGYDP-----FDVWGIG 111

140 TTVTVSS 146
112 TTVTVSS 118

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RESULT 22
HV10_MOUSE STANDARD; PRT; 117 AA.
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RX MEDLINE=81234548; PubMed=6780376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL: J00333; AAA38602.1; -.
CC PIR: C90809; HVMS45.
CC HSSP: P01810; 2FBJ.
CC MGD: MGI:96486; Igh-VJ558.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGv; 1.
CC PROSITE: PS00835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match
Best Local Similarity 43.8%; Score 347; DB 1; Length 117;
Matches 63; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 1 MEWSVFLFFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWSCIMFLAATATGVHSPVQLQPGAEVLKPGASVKLSKASGYTFTSYMHWVKQRP 60
QY 61 GORFEWGWINPYNGNKEFSKAFQDRVTFADTSANTAYMELSLRSADTAVYYCAR 117
DB 61 GRGLEWIGNIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSLTSSEDSAVYYCAR 117

RESULT 23
HV1A_HUMAN STANDARD; PRT; 117 AA.
ID HV1A_HUMAN
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90563; GIHUEU.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 43.0%; Score 341; DB 1; Length 117;
Best Local Similarity 60.9%; Pred. No. 5.3e-28;
Matches 78; Conservative 7; Mismatches 31; Indels 12; Gaps 3;

QY 20 QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPQRFWMGWINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPGSSVKSCASGCTFSRSALINVRQAPGQGLEWMGIVPMFGPPNY 60
QY 80 SAKFQDRVTADTSANTAYMELSLRSADTAVYCA-RVGPYSWDDSDPDNYYNDVWGK 138
DB 61 AOKFQGRVTITADESTNTAYMELSLRSADTAVYCA-RVGPYSWDDSDPDNYYNDVWGK 138
QY 139 GTTVIVSS 146
DB 110 GGLVTWSS 117

RESULT 24
HV1F HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region Mot.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

Query Match 43.0%; Score 341; DB 1; Length 117;
Best Local Similarity 60.9%; Pred. No. 5.3e-28;
Matches 78; Conservative 7; Mismatches 31; Indels 12; Gaps 3;

QY 20 QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPQRFWMGWINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPGSSVKSCASGCTFSRSALINVRQAPGQGLEWMGIVPMFGPPNY 60
QY 80 SAKFQDRVTADTSANTAYMELSLRSADTAVYCA-RVGPYSWDDSDPDNYYNDVWGK 138
DB 61 AOKFQGRVTITADESTNTAYMELSLRSADTAVYCA-RVGPYSWDDSDPDNYYNDVWGK 138
QY 139 GTTVIVSS 146
DB 110 GGLVTWSS 117

RESULT 24
HV1F HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region Mot.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=86203277; PubMed=3084950;
RA Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RT immunoglobulin (Mot) having unusual papain cleavage sites.";
RL Mol. Immunol. 23:169-174(1986).
DR PIR; A02025; HVHUMO.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_v.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT MOD RES 99 107 D SEGMENT.
FT DISULFID 108 125 J SEGMENT.
FT NON TER 122 96 BY SIMILARITY.
FT SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 42.7%; Score 339; DB 1; Length 125;
Best Local Similarity 52.8%; Pred. No. 9.1e-28;
Matches 67; Conservative 19; Mismatches 39; Indels 2; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPQRFWMGWINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPGSSVKSCASGDDFNFYDHWVRQAPGQGLEWMVAVFSPDRITY 60
QY 80 SAKFQDRVTADTSANTAYMELSLRSADTAVYCA-RVGPYSWDDSDPDNYYNDVWGK 139
DB 61 GPRSQARFTVTRDSTTTVMELTALISADTAIYVCARGAHYS--DTDDSGTSLGPWQGG 118
QY 140 TTVIVSS 146
DB 119 TLLIVSS 125

RESULT 25
HV00 MOUSE STANDARD; PRT; 114 AA.
ID HV00 MOUSE
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsonate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=1095336;
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

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KW Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 41.4%; Score 328.5; DB 1; Length 114;
Best Local Similarity 54.8%; Pred. No. 9.7e-27;
Matches 68; Conservative 19; Mismatches 26; Indels 11; Gaps 2;

QY 20 QVOLVQSGAEVKKPGASVKVSQCOASGYRFSNFVHVRQAPGQRFWMGWINPYNGKKEF 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 1 EVQIQQSGAEVLRGTSVKLSCKAAGTFTFYVIGWVKERPGHLEWIGDIYPCGGFTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGK 138
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 61 AQKQFQGRVTITADTSNTAYMELSSLRSDTAVYFCARV-----ISRYFDGQG 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 139 GTTV 142
D 111 GTLV 114

RESULT 26
HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6253904;
RX MEDLINE=81053741;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVMS11.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AF3BC5ED0BF CRC64;

Query Match 40.5%; Score 321; DB 1; Length 121;
Best Local Similarity 49.6%; Pred. No. 6.1e-26;
Matches 63; Conservative 26; Mismatches 32; Indels 6; Gaps 3;

QY 20 QVOLVQSGAEVKKPGASVKVSQCOASGYRFSNFVHVRQAPGQRFWMGWINPYNGKKEF 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 1 EAQIQQSGAEVLRGTSVKLSCKAAGTFTFYVIGWVKERPGHLEWIGDIYPCGGFTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 SAKFQDRVTFTADTSANTAYMELRSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGK 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 61 NDNLKGRATLTADTSSTAVYQLSSLTSDSAIYHCAH-GIY-YNSSP-----YFDSWGQG 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 140 TTVIVSS 146

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Db 115 TTVIVSS 121
||: |||

RESULT 27
HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6788376;
RX MEDLINE=81234548;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
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DR EMBL; J00522; A015290.1; -
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON TER 1 16
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 39.9%; Score 316.5; DB 1; Length 136;
Best Local Similarity 43.9%; Pred. No. 2e-25;
Matches 61; Conservative 27; Mismatches 44; Indels 7; Gaps 1;

QY 8 LFFLVTTGVHSQVLQVSGAEVKKPGASVKVSQCOASGYRFSNFVHVRQAPGQRFWM 67
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 5 VFLVILKGVQCDVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMWVWQAPKGLWV 64
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 GWINPYNGKFSKAFQDRVTFTADTSANTAYMELRSLRSADTAVVYCARVGPYSWDDSP 127
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
D 65 AVTSSGSSTLHVADTVKGRFTISRDNPNTFLQMTSLRSDTAVVYCARWGNYPY---- 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 128 QDNYMDVWGKGTIVVSS 146
DB 121 ---YMDYWGQGTIVTSS 136

RESULT 28
HV28_MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02078; AVMST6.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR DOMAIN 1 112 IG-LIKE.
FT NON TER 119
FT SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 39.3%; Score 311.5; DB 1; Length 119;
Best Local Similarity 44.9%; Pred. No. 5.6e-25;
Matches 57; Conservative 26; Mismatches 35; Indels 9; Gaps 1;

QY 20 QVOLVSGAEVKPGASVKVSQASGYRFSNFIHVRQAPGQRFQRMWGNINPYNKKEF 79
DB 1 EVKLIESGGLVPGGSLKLSCAASGDFSRYMWSVRQAPGKLEWIGEINPDSSTINY 60
QY 80 SAKFQDRVTFTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGK 139
DB 61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYG-----YFDVWGAG 111
QY 140 TTVIVSS 146
DB 112 TTVTVSS 118

RESULT 29
HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101208;

RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes."
RN Cell 27:573-581(1981).
RP SEQUENCE OF 20-142.
RX MEDLINE=7622762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS PHOSPHORYLCHOLINE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC EMBL; J00516; AAC18867.2; ALT_TERM.
DR PIR; A90818; AVMS67.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.
FT DOMAIN 20 133 IG-LIKE.
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT NON TER 144
FT SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;

Query Match 38.1%; Score 302.5; DB 1; Length 144;
Best Local Similarity 40.9%; Pred. No. 5.8e-24;
Matches 61; Conservative 31; Mismatches 44; Indels 13; Gaps 5;

QY 3 W-SVFLPFLSVTTGVISQVLVSGAEVKPGASVKVSQASGYRFSNFIHVRQAPG 61
DB 4 WLNWFL--LTLTGLGICEVKVSGGLVQPGSLKLSCATSGFTSDFDFMEVWVROTPG 61
QY 62 QRFWM--GWINPYNGNKEFSAKFQDRVTFTADTSANTAYMELRSADTAVYCARVG 119
DB 62 KRLWIAASRSKADHYRTEYSASVKGRTIVSRDTSQSVLYLQWNALEADTATYYCTRDA 121
QY 120 PYSWDDSPQDNY--YMDVWGKGTIVVSS 146
DB 122 DYG-----NSYFGYFDVWGAGTTTVSS 144

RESULT 30
HV16_HUMAN STANDARD; PRT; 124 AA.
AC P01761;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82045599; PubMed=7028111;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of heavy chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
```

RT group.";
RL Biochemistry 20:5822-5830(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02044; MHUS1.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13732 MW; 62CED4573BDEF59F CRC64;

Query Match 37.6%; Score 298.5; DB 1; Length 124;
Best Local Similarity 51.1%; Pred. No. 1.2e-23;
Matches 67; Conservative 16; Mismatches 35; Indels 13; Gaps 5;

Qy 20 QVQLVQSGAEVKKPGASVKVSQASGYRPSNFIHWVRQAPGQRFWMG-----WINPYNG 75
Db 1 QVQLVQSGAEVKKPGSSVRVTCTSGTFSGYTISWVRQAPGRLGWGSPAKWTDPFQ 60
Qy 76 NKEFSAKFDORVFTADTSANTAYMELRLSADTAIVYICARVGPYSWDDSPQDNYMDV 135
Db 61 ---VYIKW-ERVTVSLKPSFNQAYMELVNLFNEDGAVYICAR----EWKGVNVPF-DY 111
Qy 136 WGKGTTIVSS 146
Db 112 WGQGLVTSS 122

Search completed: August 26, 2004, 13:38:02
Job time : 9.65185 secs

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:34:32 ; Search time 14.0593 Seconds
(without alignments)
998.912 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MWSWVFLFSLVTVGVHSQ.....PODNYMDVWGKGTIVVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 78: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	63.2	148	2 S29257	Ig heavy chain V r
2	496	62.5	127	2 S14683	Ig mu chain precu
3	483	60.9	117	2 S18553	Ig heavy chain V r
4	478.5	60.3	136	2 S38600	Ig heavy chain V r
5	477.5	60.2	135	2 S49530	anti-Sm antibody V
6	475.5	60.0	171	2 S23623	Ig heavy chain V r
7	469	59.1	129	2 S46393	Ig heavy chain V r
8	469	59.1	160	2 PL0105	anti-PR2 erythrocy
9	467	58.9	117	2 S18552	Ig heavy chain V r
10	463	58.4	129	2 S38260	Ig heavy chain V r
11	453	57.1	117	2 S18551	Ig heavy chain V r
12	452.5	57.1	124	2 S19665	Ig heavy chain V r
13	452.5	57.1	143	1 E1HUND	Ig heavy chain V r
14	450	56.7	131	2 S21924	Ig heavy chain V r
15	449	56.6	117	2 S31680	Ig heavy chain V r
16	448.5	56.6	139	2 A27609	Ig heavy chain V r
17	444.5	56.1	474	1 G2MS11	Ig gamma-2b chain
18	443.5	55.9	139	2 FS0024	Ig heavy chain pre
19	442.5	55.8	132	2 S31596	Ig heavy chain V r
20	441	55.6	140	2 PH1482	Ig heavy chain V r
21	438.5	55.3	133	2 PC1155	Ig heavy chain pre
22	437	55.1	123	2 D33518	Ig heavy chain V-1
23	437	55.1	142	2 S19245	Ig heavy chain pre
24	436.5	55.0	118	2 S38265	Ig heavy chain V r
25	433.5	54.7	118	2 PH1666	Ig heavy chain V r
26	433.5	54.7	469	2 S37483	Ig gamma-2a chain
27	433	54.6	117	1 HVHUS3	Ig heavy chain pre
28	433	54.6	133	2 C33548	Ig heavy chain V-1
29	432.5	54.5	137	2 H32513	Ig heavy chain pre

30	432	54.5	142	2 A32483	Ig heavy chain V r
31	431	54.4	117	1 HVHUSG	Ig heavy chain pre
32	430	54.2	140	2 PH1498	Ig heavy chain V r
33	429	54.1	140	2 T01407	Ig heavy chain (my
34	428	54.0	127	2 PH0955	Ig heavy chain V r
35	427	53.8	134	2 S21916	Ig heavy chain V r
36	426.5	53.8	116	2 S31657	Ig heavy chain V r
37	426.5	53.8	135	2 PS0057	Ig heavy chain pre
38	426	53.7	117	2 PT0371	Ig gamma chain pre
39	426	53.7	140	2 PH1484	Ig heavy chain V r
40	425	53.6	111	2 S21925	Ig heavy chain V r
41	425	53.6	135	2 PH1493	Ig heavy chain V r
42	425	53.6	140	2 PH1489	Ig heavy chain V r
43	424	53.5	140	2 PH1488	Ig heavy chain V r
44	423.5	53.4	114	2 PH1667	Ig heavy chain V r
45	423	53.3	140	1 HVMSG7	Ig heavy chain pre
46	421	53.1	136	2 S04576	Ig heavy chain pre
47	420	53.0	122	2 S36271	Ig heavy chain V r
48	420	53.0	140	2 PH1483	Ig heavy chain V r
49	419	52.8	140	2 PH1486	Ig heavy chain V r
50	418.5	52.8	132	2 S46394	Ig heavy chain V r
51	418	52.7	138	2 S21810	Ig heavy chain V r
52	417.5	52.6	150	2 PN0444	Ig heavy chain V r
53	416	52.4	127	2 S34014	Ig heavy chain V r
54	415.5	52.4	126	2 B33548	Ig heavy chain V-1
55	415.5	52.4	132	2 PH0954	Ig heavy chain V r
56	414.5	52.3	135	2 B32274	Ig heavy chain pre
57	414.5	52.3	141	2 A39276	Ig heavy chain pre
58	413	52.1	166	2 PL0012	Ig heavy chain pre
59	412	52.0	119	2 PH0961	Ig heavy chain pre
60	410	51.7	117	2 S18554	Ig heavy chain V r
61	410	51.7	131	2 S26792	Ig heavy chain V r
62	410	51.7	135	2 PH1492	Ig heavy chain V r
63	410	51.7	151	2 PL0011	Ig heavy chain pre
64	409.5	51.6	122	2 PH0958	Ig heavy chain V r
65	409.5	51.6	128	2 PH0952	Ig heavy chain V r
66	409.5	51.6	137	2 S52445	Ig heavy chain V r
67	409	51.6	135	2 PH1494	Ig heavy chain V r
68	408.5	51.5	139	1 MHMS18	Ig heavy chain pre
69	407.5	51.4	141	2 JL0076	Ig heavy chain pre
70	405.5	51.1	136	2 PH0960	Ig heavy chain V r
71	404.5	51.0	120	2 S31999	Ig heavy chain V r
72	403.5	50.9	116	2 S31698	Ig heavy chain pre
73	403	50.8	125	2 PH0957	Ig heavy chain V r
74	403	50.8	138	2 E32513	Ig heavy chain pre
75	402	50.7	117	1 HVMS8A	Ig heavy chain pre
76	401	50.6	121	2 S20783	Ig heavy chain pre
77	400	50.4	126	2 I44151	Ig heavy chain V r
78	399	50.3	138	2 PH0105	anti-digoxin trans
79	398.5	50.3	137	2 C41287	Ig heavy chain V r
80	398	50.2	98	2 S26919	Ig heavy chain V r
81	398	50.2	135	2 PH0953	Ig heavy chain V r
82	398	50.2	136	2 S35759	BHD9D1.0 protein -
83	395	49.8	121	2 A49590	Ig heavy chain V r
84	394.5	49.7	116	2 PH0959	Ig heavy chain V r
85	394.5	49.7	146	4 S33905	Ig heavy chain pre
86	394	49.7	140	2 PH1499	Ig heavy chain V r
87	394	49.7	140	2 A36194	Ig heavy chain V r
88	392.5	49.5	104	2 PH1665	Ig heavy chain V r
89	392.5	49.5	147	2 PH1561	Ig heavy chain V r
90	391.5	49.4	135	2 A30577	Ig heavy chain pre
91	391.5	49.4	137	1 G2MS43	Ig heavy chain pre
92	391	49.3	98	2 S26938	Ig heavy chain V r
93	390.5	49.2	120	2 PH0962	Ig heavy chain V r
94	389.5	49.1	122	2 PH0887	Ig heavy chain V r
95	389	49.1	131	2 A27472	Ig heavy chain pre
96	389	49.1	138	1 HVMS7	Ig heavy chain pre
97	388	48.9	136	2 FL0208	Ig heavy chain pre
98	387.5	48.9	178	2 S29594	Ig gamma chain (WM
99	387	48.8	125	2 S68170	Ig heavy chain V r
100	387	48.8	129	2 A33548	Ig heavy chain V-1

ALIGNMENTS

RESULT 1

S29257
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouhan, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a (D)H segment
A:Reference number: S29257; MUID:9236264; PMID:1499555
A:Accession: S29257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:542403; NID:9253699; PIDN:BA82940.1; PID:G253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.2%; Score 501; DB 2; Length 148;
Best Local Similarity 62.2%; Pred. No. 2e-38;
Matches 97; Conservative 15; Mismatches 26; Indels 18; Gaps 2;
QY 1 MEWSWVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQPEWGWINPYNGNKEFSAKQDRTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQSLWNGHISVADGKTKYQKQDRTITRDTSAITAYMEVGLSRSEDATVYICAR--- 117

QY 121 YSWDDSPQDNY-----YMDVWKGTTIVVSS 146
DB 118 -----SPRINWVRGLITTPFPFDSMGQGLIVVSS 148

RESULT 2

S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <PRI>
A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 496; DB 2; Length 627;
Best Local Similarity 65.1%; Pred. No. 2.5e-37;
Matches 99; Conservative 15; Mismatches 32; Indels 6; Gaps 2;
QY 1 MEWSWVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRFLVAAATGVHSGVQLVQSGAEVKKPGSSVKVSQASGGTFFSYALSWVRQAP 60
QY 61 GQPEWGWINPYNGNKEFSAKQDRTFTADTSANTAYMELSLRSADTAVYICAR--- 117
DB 61 GQGLEWNGGIPIFGTANYAKQFGRTITADSTSTAYMELSLSRSEDATVYICARTGI 120
QY 118 VGPYSMDPSQDNY---MDVWKGTTIVVSS 146
DB 121 LGPYSGWYNSDYIYGVMDVWVGQTTIVVSS 152

RESULT 3

S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18553; S26516
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18553
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62109
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26916
A:Molecule type: DNA
A:Residues: 20-117 <TOM>
A:Cross-references: EMBL:Z12327; NID:G32871; PIDN:CAA78197.1; PID:G32872
C:Genetics:
A:Introns: 16/1
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 60.9%; Score 483; DB 2; Length 117;
Best Local Similarity 75.2%; Pred. No. 6.7e-37;
Matches 88; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 1 MEWSWVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAAATGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQPEWGWINPYNGNKEFSAKQDRTFTADTSANTAYMELSLRSADTAVYICAR 117
DB 61 GQLEWNGWINAGNNTKYQKQDRTITRDTSAITAYMELSLSRSEDATVYICAR 117

RESULT 4

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 478.5; DB 2; Length 136;
Best Local Similarity 62.3%; Pred. No. 2e-36;
Matches 91; Conservative 18; Mismatches 26; Indels 11; Gaps 2;
QY 1 MEWSWVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAAATSAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAT 60

Query Match	60.0%; Score 475.5; DB 2; Length 171;
Best Local Similarity	62.4%; Pred.No. 4.8e-36;
Matches 93; Conservative 15; Mismatches 34; Indels 7; Gaps 3;	
OY	1 MEMSWFLFLLSVTTGVHSGVOLVQSGAEVKPGASVKVSCKGSGYFFSNFIHWVRQP 60
	: : : : : : : : : : : : : : : : : :
Db	1 MDWTWRLLFLVAATAGHSVOLVQSGAEVKPGASVKVSCKGSGYFTTAYQHWRQP 60
	: : : : : : : : : : : : : : : : : :
OY	61 GQPFKMGWINPYNGNKEFKSAKFODRYTFTADTSANTAYMELSLRSADTAIVYCARGVP 120
	: : : : : : : : : : : : : : : : : :

QV 1 MEWSWVLFELSLVTGTGHSOVOLVOSGAEVKKPGASVKVSCOASGYRFSNFVIHWVROAP 60

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Db      1 MDWTSLFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAP 60
QY      61 GQPEFWGWINPYNGKNEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYICARV-- 118
Db      61 GQGLEWGWISVYNGDNTYNAQNLQGRVTFTDTSANTAYMELSLRSDDTAVYICARPG 120
QY      119 -----GFYSWDDSPQDNYNMDVWGKGTIVVSS 146
Db      121 YCSGGGCGYRD-----DYWGQGLTVTVSS 144

RESULT 9
S18552
Ig heavy chain V region precursor (VI-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18552
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18552
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62107; NID:g37833; PIDN:CAA44017.1; PID:g37834
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:119/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      58.9%; Score 467; DB 2; Length 117;
Best Local Similarity 72.6%; Pred. No. 1.9e-35;
Matches 85; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY      1 MENSWVFLFSLVTGTGHSQVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAP 60
Db      1 MDWTRILFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAP 60
QY      61 GQPEFWGWINPYNGKNEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYICAR 117
Db      61 GQRLWGWGNSAGNTKYQCFQGRVTITRDTASANTAYMELSLRSDDTAVYICAR 117

RESULT 10
S36260
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36260
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36260
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-129 <GRI>
A:Cross-references: EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g9939903
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      58.4%; Score 463; DB 2; Length 129;
Best Local Similarity 71.3%; Pred. No. 4.8e-35;
Matches 92; Conservative 8; Mismatches 27; Indels 1; Gaps 1;

QY      20 QVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKNEF 79

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Db      1 QVQLQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWGMHISAYNGNTY 60
QY      80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYICAR--VGYPYWDSPQDNYNMDVWG 137
Db      61 AQKLGQRTMTDTSANTAYMELSLRSDDTAVYICARSDSGYCSSTSCFYVYVMDVWG 120
QY      138 KGTIVVSS 146
Db      121 KGTIVTVSS 129

RESULT 11
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S23625
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
R:Olse, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.; C
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv
A:Reference number: S23623; MUID:92156804; PMID:11740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      57.1%; Score 453; DB 2; Length 117;
Best Local Similarity 70.1%; Pred. No. 3.5e-34;
Matches 82; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY      1 MENSWVFLFSLVTGTGHSQVQLVQSGAEVKKPGASVKVSCKASGYRFSNFIHWVRQAP 60
Db      1 MDWTRILFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTGYVHWVRQAP 60
QY      61 GQPEFWGWINPYNGKNEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYICAR 117
Db      61 GQGLEWGWINPNSGGTNYAQCFQGRVTMTTRDTSIANTAYMELSLRSDDTAVYICAR 117

RESULT 12
S19665
Ig heavy chain V region (alpha-phOx15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C:Accession: S19665; S24442
R:Marks, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19665
A:Molecule type: mRNA
A:Residues: 1-124 <MAR>
A:Cross-references: EMBL:X61647
R:Jones, P.T.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24442
A:Accession: S24442
A:Molecule type: mRNA

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A;Residues: 1-40.'GLSGWDGSAITMTVQSILDK' 61-118.'T'.120-124 <JON>
A;Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g1335368
A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the s
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.1%; Score 452.5; DB 2; Length 124;
Best Local Similarity 69.3%; Pred. No. 4.2e-34;
Matches 88; Conservative 13; Mismatches 23; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAPGQRFEMMGWINPYNGNKEF 79
Db 1 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAPGQRFEMMGWINPYNGNKEF 60

QY 80 SAKFDQRTVTTADTSANTAYMELRSADTAVYCARVGPYSWDSQPDNYVMYDWGKG 139
Db 61 AQLQGRVTMTDTSTSTAYMELRSDDTAVYCVRLLP---KRTATLEYIDVWGKG 117

QY 140 TTVIVSS 146
Db 118 TLTVSS 124

RESULT 13
ElHUND
Ig heavy chain precursor V-I region (Nd) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C;Accession: A93933; A02026
R;Kanten, J.H.; Wolgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A;Reference number: A93933; MUID:83065234; PMID:6815656
A;Accession: A93933
A;Molecule type: mRNA
A;Residues: 1-143 <XEN>
R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A;Reference number: A94418
A;Contents: annotation; partial sequence
A;Note: this epsilon chain was isolated from a myeloma protein
C;Genetics:
A;Gene: IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
F;35-113/Domain: immunoglobulin homology <IMM>
F;16/Modified site: pyroglutamic carboxylic acid (Gln) (in mature form) #status experime
F;37-111/Disulfide bonds: #status experimental

Query Match 57.1%; Score 452.5; DB 1; Length 143;
Best Local Similarity 58.1%; Pred. No. 4.8e-34;
Matches 86; Conservative 24; Mismatches 31; Indels 7; Gaps 3;

QY 1 NEWSWVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
Db 1 MDWT---FLVAATRVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 56

QY 61 GQRFEMMGWINPYNGNKEFSADTAVYCARVGPYSWDSQPDNYVMYDWGKG 120
Db 57 CHGLEWGWINPNSGGTNYAPRQGRVTMTDRASFSTAYMELRSDDSAFVYCAKSP 116

QY 121 YSWDD--SPQDNYVMYDWGKGTTIVSS 146
Db 117 F-MSDYNYFDYSYTLDWGQGTIVTVSS 143

RESULT 14
S21924

Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21924; S21923
R;Friedman, D.F.
submitted to the EMBL Data Library, July 1991
A;Reference number: S21923
A;Accession: S21924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <FRI>
A;Cross-references: EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID:g33566; EMBL:X60504; N
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 56.7%; Score 450; DB 2; Length 131;
Best Local Similarity 68.6%; Pred. No. 7.4e-34;
Matches 83; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 1 NEWSWVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
Db 1 MDWTWSILFLVAATGAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60

QY 61 GQRFEMMGWINPYNGNKEFSADTAVYCARVGPYSWDSQPDNYVMYDWGKG 120
Db 61 GQGLEWGWINPNSGGTNYAQLQGRVTMTDTSTAYMELRSDDTAVYCARAPG 120

QY 121 Y 121
Db 121 Y 121

RESULT 15
S31680
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31680
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the i
A;Reference number: S31585
A;Accession: S31680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CU>
A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 56.6%; Score 449; DB 2; Length 117;
Best Local Similarity 69.2%; Pred. No. 8.2e-34;
Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 NEWSWVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
Db 1 MDWTWRVFLVAATGAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60

QY 61 GQRFEMMGWINPYNGNKEFSADTAVYCARVGPYSWDSQPDNYVMYDWGKG 117
Db 61 GQGLEWGWINPNSGGTNYAQLQGRVTMTDTSTAYMELRSDDTAVYCAR 117

RESULT 16
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
A/Accession: A27609
R/Klein, D.; Nietupski, J.; Sirlin, S.; Stavner, J.
J. Immunol. 140, 1578-1584, 1988
A/Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A/Reference number: A27609; MUID:88154467; PMID:3126234
A/Accession: A27609
A/Molecule type: DNA
A/Residues: 1-139 <KLE>
A/Cross-references: EMBL:M19401; MID:G195441; PIDN:AAA38303.1; PID:G553992
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 56.6%; Score 448.5; DB 2; Length 139;
Best Local Similarity 56.8%; Pred. No. 1.1e-33;
Matches 83; Conservative 25; Mismatches 31; Indels 7; Gaps 1;

Qy/ 1 MWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPKASVKSCASQSVKPSVNFVHWRQAP 60
Db 1 MGWVIFLLSGTAGVSEVQLQSGPELVKPGASVMSCKASGTFDDYVHWKQSN 60

Qy 61 GQREPMWGWNPYNGNKEFSKAFQDRVTFADTSANTAYMELSLRSADTAVYVCARVGP 120
Db 61 GKSLEWIGYINPYNDYTSYQKPKGKATLVKSSSTAYVQLNSLTSEDSAVYVCARYS 120

Qy 121 YSWDDSPQDNYMVDWVGKGTIVVSS 146
Db 121 YSY-----YAMDYWGQGTIVTVSS 139

RESULT 17
G2MS11
Ig gamma-2b chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C/Accession: S25057; A02157; A26235; A26233; A53598
R/Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
Submitted to the EMBL Data Library, July 1992
A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A/Reference number: S25057
A/Accession: S25057
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-474 <FIS>
A/Cross-references: EMBL:X67210; MID:954826; PIDN:CAA47649.1; PID:G54827
R/Yanawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A/Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
A/Reference number: A02157; MUID:80120716; PMID:6766534
A/Contents: a allele
A/Accession: A02157
A/Molecule type: DNA
A/Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A/Cross-references: GB:J00461
A/Note: the sequence was determined from the germline gene
R/Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A/Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A/Reference number: A26235; MUID:80081501; PMID:117548
A/Contents: MPC 11
A/Accession: A26235
A/Molecule type: mRNA
A/Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A/Note: Lys-474 is probably removed posttranslationally
R/Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A/Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
A/Reference number: A26232; MUID:80081502; PMID:117549

A/Accession: A26232
A/Molecule type: DNA
A/Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
R/Ollo, R.; Rougeon, F.
Nature 296, 763-763, 1982
A/Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
A/Reference number: A26233; MUID:82173203; PMID:6803173
A/Contents: b allele
A/Accession: A26233
A/Molecule type: DNA
A/Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
A/Cross-references: GB:J00461
R/Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
J. Biol. Chem. 269, 12345-12350, 1994
A/Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A/Reference number: A53598; MUID:94216359; PMID:7512967
A/Accession: A53598
A/Status: preliminary
A/Molecule type: protein
A/Residues: 234-251 <KIM>
C/Comment: The a allele sequence is shown.
C/Genetics:
A/Introns: 138/1; 236/1; 258/1; 368/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul
F:157-222/Domain: immunoglobulin homology <IM1>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220, 288-348, 394-452/Disulfide bonds: #status predicted
F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.1%; Score 444.5; DB 1; Length 474;
Best Local Similarity 56.8%; Pred. No. 8.8e-33;
Matches 83; Conservative 19; Mismatches 35; Indels 9; Gaps 1;

Qy 1 MWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPKASVKSCASQSVKPSVNFVHWRQAP 60
Db 1 MGWVIFLLSGTAGVSEVQLQSGPELVKPGASVMSCKASGTFDDYVHWKQSN 60

Qy 61 GQREPMWGWNPYNGNKEFSKAFQDRVTFADTSANTAYMELSLRSADTAVYVCARVGP 120
Db 61 GQLEWIGYINPYNDYTSYQKPKGKATLVKSSSTAYVQLNSLTSEDSAVYVCARDYD 120

Qy 121 YSWDDSPQDNYMVDWVGKGTIVVSS 146
Db 121 YDW-----FAYWGQGTIVTVSA 137

RESULT 18
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C/Accession: PS0024
R/Margat, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A/Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A/Reference number: PS0023; MUID:89232725; PMID:3149944
A/Accession: PS0024
A/Molecule type: mRNA
A/Residues: 1-139 <MAR>
A/Experimental source: strain BALB/c
C/Comment: this chain is obtained from an IgG2a monoclonal antibody against Pseudomonas
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-13/Domain: signal sequence #status predicted <SIG>
F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F:34-117/Domain: immunoglobulin homology <IMM>

F:20/Modified site: pyroliadone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 55.8%; Score 442.5; DB 2; Length 132;
Best Local Similarity 58.2%; Pred. No. 3.6e-33;
Matches 85; Conservative 17; Mismatches 29; Indels 15; Gaps 1;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAP 60
DB 1 MEWHIFLFLSVTAGVHSEVQLQOQSGAEVLRAGSSVKMSCKASGYTFTSYGINWVKQRP 60
QY 61 GORFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWIGYINPGNGYTKYNEKFKGKTTLTVDKSSSTAYMQLSLTSDSAVYFCARVY 117
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 118 -----SYNYEGAMDYWGQGTIVVSS 139

RESULT 19
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Guisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CU1>
A:Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 55.8%; Score 442.5; DB 2; Length 132;
Best Local Similarity 58.2%; Pred. No. 3.6e-33;
Matches 85; Conservative 17; Mismatches 29; Indels 15; Gaps 1;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAP 60
DB 1 MDWTRILFLVAATSAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDLDWRQAT 60
QY 61 GORFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 118
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 119 -----PAMQGTMTVTVSS 131

RESULT 20
PH1482
Ig heavy chain V region (clones 36-35[IG] and X7-TC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1482; PH1495
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1482
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GU>
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1

F:20/Modified site: pyroliadone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 55.6%; Score 441; DB 2; Length 140;
Best Local Similarity 56.2%; Pred. No. 5.2e-33;
Matches 82; Conservative 28; Mismatches 30; Indels 6; Gaps 1;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAP 60
DB 1 MEWSVFLFSLVTTGVHSEVQLQOQSGAEVLRAGSSVKMSCKASGYTFTSYGINWVKQRP 60
QY 61 GORFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWIGYINPGNGYTKYNEKFKGKTTLTVDKSSSTAYMQLSLTSDSAVYFCARVY 120
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 121 YG-----GSYFDYWGQGTIVVSS 140

RESULT 21
PC1155
Ig heavy chain precursor V region (B72.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PC1155
R:Whittle, N.; Adair, J.; Lloyd, C.; Jenkins, L.; Devine, J.; Schlom, J.; Raubitschek, A.
Protein Eng. 1, 499-505, 1987
A:Title: Expression in COS cells of a mouse-human chimaeric B72.3 antibody.
A:Reference number: PC1155; MUID:89220990; PMID:3508296
A:Accession: PC1155
A:Molecule type: mRNA
A:Residues: 1-133 <WH1>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-133/Product: Ig heavy chain V region (B72.3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 55.3%; Score 438.5; DB 2; Length 133;
Best Local Similarity 57.5%; Pred. No. 8.3e-33;
Matches 84; Conservative 23; Mismatches 26; Indels 13; Gaps 2;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAP 60
DB 1 MEWSVFLFSLVTTGVHSGVQLQOQSGAEVLRAGSSVKMSCKASGYTFTDHAHWAKQXP 60
QY 61 GORFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWIGYISPGNDIKYNEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARVY 117
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 118 -----SYY-GHWGQGTIVVSS 133

RESULT 22
D33548
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene ex-
pression in B cell leukemia.
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: D33548
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.1%; Score 437; DB 2; Length 123;
Best Local Similarity 66.9%; Pred. No. 1.1e-32;
Matches 85; Conservative 9; Mismatches 29; Indels 4; Gaps 1;

QY 20 QVQLVQSGAEVKKPKGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPKGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEF 79

QY 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGYSDWDDSPQD--NYMDVWG 139
DB 61 AEKFGQRTVITRDTSINTAYMELSLRSDDTAVYCARASYCYGD----CYFFDYWGQ 116

QY 140 TTVIVSS 146
DB 117 TLTVSS 123

RESULT 23

S19245
Ig heavy chain precursor V region (10P1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S19245
R:Kirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
EMBO J. 11, 603-609, 1992
A:Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure
A:Reference number: S19245; MUID:92164649; PMID:1537339
A:Accession: S19245
A:Status: Preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-142 <KIR>
A:Cross-references: EMBL:X59906; NID:G37791; PIDN:CAA42547.1; PID:G37792
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 55.1%; Score 437; DB 2; Length 142;
Best Local Similarity 53.2%; Pred. No. 1.2e-32;
Matches 82; Conservative 21; Mismatches 31; Indels 20; Gaps 2;

QY 1 MEWSWFLPFLSVTTGVHSGVQLVQSGAEVKKPKGASVKVSCQASGYRFSNFIHWVRQAP 60
DB 1 MDWTIRILFLVAATGAHSGVQLVQSGAEVKKPKGASVKVSCQASGYRFSNFIHWVRQAP 60

QY 61 GQFQFWMGWINPYNGNKEFSAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGP 120
DB 61 GQFQFWMGWINTGNPTFAQGTGRVFSLDTSVSTAYLQISLRAEDTAVYCARA-- 118

QY 121 YSWDDSPQDNY-----YMDVWGKGTIVVSS 146
DB 119 -----YTLMTAVTHDFWGGTLTVVSS 142

RESULT 24

S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679590
A:Accession: S36265
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>
A:Cross-references: EMBL:Z18846; NID:G33121; PIDN:CAA79298.1; PID:G939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.0%; Score 436.5; DB 2; Length 118;
Best Local Similarity 66.7%; Pred. No. 1.1e-32;
Matches 86; Conservative 11; Mismatches 19; Indels 13; Gaps 2;

QY 20 QVQLVQSGAEVKKPKGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPKGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEF 79

QY 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGYSDWDDSPQD--NYMDVWG 137
DB 61 AEKFGQRTVITRDTSINTAYMELSLRSDDTAVYCARASYCYGD----CYFFDYWGQ 109

QY 138 KGTIVVSS 146
DB 110 QGTLTVSS 118

RESULT 25
PH1666
Ig heavy chain V region (clone 6C9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1666
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1666
A:Molecule type: mRNA
A:Residues: 1-118 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 54.7%; Score 433.5; DB 2; Length 118;
Best Local Similarity 70.2%; Pred. No. 2.1e-32;
Matches 85; Conservative 12; Mismatches 19; Indels 5; Gaps 2;

QY 28 AEVKKPKGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEFSAKFQDRV 87
DB 1 AEVKKPKGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEFSAKFQDRV 87

QY 88 TFTADTSANTAYMELSLRSADTAVYCARVGYSDWDDSPQDNY--MDVWGKGTIVVSS 145
DB 61 TITRDTGASTAYMELSLRSDDTAVYCARASYCYGD----CYFFDYWGQ 117

QY 146 S 146
DB 118 S 118

RESULT 26
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.P.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA9868.1; PID:G406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 54.7%; Score 433.5; DB 2; Length 469;
Best Local Similarity 54.4%; Pred. No. 8.6e-32;

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-133 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 54.6%; Score 433; DB 2; Length 133;
Best Local Similarity 66.9%; Pred. No. 2.6e-32;
Matches 89; Conservative 11; Mismatches 27; Indels 6; Gaps 2;

Qy 20 QVQLVQSGAEVKKPCASVKVSCQASGYFSPNFIHWVRQAPGCRPEWGMWNPYNGKEF 79
Db 1 QVQLVQSGAEVKKPCSSVKVSKCGGTFSSAISWVRQAPGCGLEWGGIPIFGTANY 60
Qy 80 SAKFQDQVTFADTSTANTAYMELSLRSRSDTAVVYCAR---VGPYSWDDSPQDNY---M 133
Db 61 AQKFQGRVTTTADGSTSTAYMELSLRSRSDTAVVYCAKTGILGYPYSSGWPNSDYYVGM 120
Qy 134 DWVGKGTTVIVSS 146
Db 121 DWVGQGTTVIVSS 133

RESULT 29
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; I
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: GB:M20831; NID:G196949; PIDN:AAA38848.1; PID:G196950
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 54.5%; Score 432.5; DB 2; Length 137;
Best Local Similarity 54.7%; Pred. No. 3e-32;
Matches 81; Conservative 25; Mismatches 29; Indels 13; Gaps 2;

Qy 1 MEWSWVFLFLSVTTGTHSQVLVQSGAEVKKPGASVKVSCQASGYRFPNFIHWVRQAP 60
Db 1 MGWSWIFLFLSVTAGVHSEIQLQSGAELKPGASVKISCKASGYSTFTYNNWVYKQSH 60
Qy 61 GQRPEWGMWNPYNGKNEFSAKFQDRVTFADTSTANTAYMELSLRSADTAVVYCARVGP 120
Db 61 GKSLWETGNINPYGTSYVQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVVYCAR--- 117
Qy 121 YSWDDSPQDNY--YMDVWGKGTTVIVSS 146
Db 118 -----KNYGSFDYWGQGTTLTVSS 137

RESULT 30
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usin
A;Reference number: A32483; MUID:69273586; PMID:2499327
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

Query Match 54.5%; Score 432; DB 2; Length 142;
Best Local Similarity 59.1%; Pred. No. 3.5e-32;
Matches 88; Conservative 10; Mismatches 25; Indels 26; Gaps 2;
Qy 11 LSVTTGVHSGVQLVQSGAEVKKFGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEMGWI 70
Db 2 LAVAPGAHSQVQLVQSGAEVKKFGASVKVSCRAAGVTFTNYMHWVRQAPGQGLEWVGII 61
Qy 71 NPYNGNKFSAKPDQDRVTFTADTSANTAYMELSLRSADTAVYCAR----- 117
Db 62 NPSGNTNYAQKFGQGVTVTRDTSTVYMEISSLRSEDVAVYCARLATTIFGVLI 121
Qy 118 VGPYSWDDSPQDNVYMDVWGKGTIVVSS 146
Db 122 TG-----MDYWGQGLTVVSS 137

Search completed: August 26, 2004, 13:39:52
Job time : 15.0593 secs